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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:57:03 ; Search time 43 Seconds
(without alignments)
401.022 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFFNRVITLTPSSDVNYS.....DAFKSPRHLPRKRHKICNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA*
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2: /cgn2_6/prodata/1/aaa/5B-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1165	100.0	231	US-10-386-972-2	Sequence 2, Appli
2	1160	99.6	231	US-08-721-259-2	Sequence 2, Appli
3	1160	99.6	231	US-09-611-216-2	Sequence 2, Appli
4	423.5	36.4	265	US-07-958-551-2	Sequence 2, Appli
5	423.5	36.4	265	US-08-129-610-7	Sequence 7, Appli
6	423.5	36.4	265	US-08-129-609A-7	Sequence 7, Appli
7	423.5	36.4	265	US-08-455-313-7	Sequence 7, Appli
8	423.5	36.4	265	US-08-475-924-2	Sequence 2, Appli
9	423.5	36.4	265	US-08-657-579A-2	Sequence 2, Appli
10	423.5	36.4	265	US-09-224-025-7	Sequence 7, Appli
11	423.5	36.4	265	US-09-706-541-7	Sequence 7, Appli
12	423.5	36.4	265	US-08-129-610-8	Sequence 7, Appli
13	417	35.8	222	US-08-129-610-8	Sequence 8, Appli
14	417	35.8	222	US-08-129-609A-8	Sequence 8, Appli
15	417	35.8	222	US-08-455-313-8	Sequence 8, Appli
16	417	35.8	222	US-08-475-924-3	Sequence 3, Appli
17	417	35.8	222	US-08-657-579A-3	Sequence 3, Appli
18	417	35.8	222	US-09-224-025-8	Sequence 8, Appli
19	417	35.8	222	US-09-706-541-8	Sequence 8, Appli
20	417	35.8	222	US-08-129-610-8	Sequence 8, Appli
21	97	8.3	1833	US-08-621-944A-4	Sequence 4, Appli
22	97	8.3	1833	US-08-945-567D-4	Sequence 4, Appli
23	97	8.3	1992	US-08-621-944A-3	Sequence 3, Appli
24	97	8.3	1992	US-08-945-567D-3	Sequence 3, Appli
25	97	8.3	2048	US-09-268-347-48	Sequence 48, Appli
26	93	8.0	2123	US-08-968-685A-10	Sequence 10, Appli
27	89.5	7.7	624	US-09-248-796A-24363	Sequence 24363, A

ALIGNMENTS

RESULT 1

US-10-386-972-2
; Sequence 2, Application US/10386972
; Patent No. 6686452
; GENERAL INFORMATION:

; APPLICANT: Rupar, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuting
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: Bacillus thuringiensis CryET29 Compositions Toxic to Coleopteran
; TITLE OF INVENTION: Insects and Ctenocephalides Spp.
; FILE REFERENCE: MECO-017--2
; CURRENT APPLICATION NUMBER: US/10/386,972
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-10-386-972-2

Query Match 100.0%; Score 1165; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-111;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MFFNRVITLTPSSDVNYSIYVAPQYVQALTLAKYFQCAIDGSLRPFDEKALQIA	60
Qy	61	NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTPT	120
Db	61	NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTPT	120
Qy	121	NLNSQSESAWIFYKEDAHKTSYYNIIILFAIQDEETGGVMATLPFAIDISVDIEKEKVLV	180
Db	121	NLNSQSESAWIFYKEDAHKTSYYNIIILFAIQDEETGGVMATLPFAIDISVDIEKEKVLV	180
Qy	181	VTIKDTENYAVTVKAINVQALQSSRDSKVVDAPFKSPRHLPRKRHKICNS	231
Db	181	VTIKDTENYAVTVKAINVQALQSSRDSKVVDAPFKSPRHLPRKRHKICNS	231

RESULT 2

US-08-721-259-2
; Sequence 2, Application US/08721259

; Patent No. 6093695
; GENERAL INFORMATION:
; APPLICANT: Rupan, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
; TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN
; TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: Concurrently Herewith
; APPLICATION NUMBER: US/08/721,259
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-721-259-2

Query Match 99.6%; Score 1160; DB 3; Length 231;
Best Local Similarity 99.6%; Pred. No. 8.6e-111;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFFNRVITLTPSSDVVNYSEIYQVAPQVYVQALTLAKYFQGAIDGSLRDFEFKALQIA 60
DB 1 MFFNRVITLTPSSDVVNYSEIYQVAPQVYVQALTLAKYFQGAIDGSLRDFEFKALQIA 60
QY 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIYDINKVLSIVIDNKKFWDQVTAITNTFT 120
DB 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIYDINKVLSIVIDNKKFWDQVTAITNTFT 120
QY 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDIEKEKVL 180
DB 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDIEKEKVL 180
QY 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
DB 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 3
US-09-611-216-2
; Sequence 2, Application US/09611216
; Patent No. 6537756
; GENERAL INFORMATION:
; APPLICANT: Rupan, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
; TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN

; TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/611,216
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,259
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-611-216-2

Query Match 99.6%; Score 1160; DB 4; Length 231;
Best Local Similarity 99.6%; Pred. No. 8.6e-111;
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFFNRVITLTPSSDVVNYSEIYQVAPQVYVQALTLAKYFQGAIDGSLRDFEFKALQIA 60
DB 1 MFFNRVITLTPSSDVVNYSEIYQVAPQVYVQALTLAKYFQGAIDGSLRDFEFKALQIA 60
QY 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIYDINKVLSIVIDNKKFWDQVTAITNTFT 120
DB 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIYDINKVLSIVIDNKKFWDQVTAITNTFT 120
QY 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDIEKEKVL 180
DB 121 NLNQSSEAWIFYKKEDAKHTSYNNILFAIQDEBTGGVMATLPIAFDISVDIEKEKVL 180
QY 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
DB 181 VTIKDTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231

RESULT 4
US-07-958-551-2
; Sequence 2, Application US/07958551
; Patent No. 5302387
; GENERAL INFORMATION:
; APPLICANT: Payne, Jewel M.
; APPLICANT: Kennedy, Keith M.
; APPLICANT: Randall, John Brookes
; APPLICANT: Brower, David Orlin
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active Against
; TITLE OF INVENTION: Cockroaches and Genes Encoding Cockroach-Active
; TITLE OF INVENTION: Toxins
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1

```
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,551
; FILING DATE: October 19, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/788,654
; FILING DATE: No. 5302387ember 6, 1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/J 101.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleonensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-07-958-551-2

Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVILTPSSDVVNYSEIQVA----POYVNOALTAKYFQAI-----DGLTLRPFDE 54
Db 38 RVILKLV--KDPIDTTQLLEITEIENPNVYLQALAAAFQDALVPTETFEGEAIRFSMP 95
Qy 55 KALQIANDI-POAAVNTLNQTVQGVSMIDKIVDMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPGAVVATDQTLSSNNQVSMIDRVISLVLTVMGVALSG-SIITQLTA 154
Qy 114 AITNTFTNLNSQESAWIPYKEDAHKTSYYNIFAIQDEETGGMATLPIAFDISVDI 173
Db 155 AITDFTNLNTQKDSAWVFWGKETSQHTNYTYNVNFAIQNETTGRVVMCVPIGEIRVET 214
Qy 174 EKEKLVFTIKDNTENYATVAVVQVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTA 220
Db 215 DKRTVLFTLTQDYANYSVNIQTLRPAQLIDSRALSINDLSALRSKYL 264

US-08-129-610-7

RESULT 5
US-08-129-610-7
; Sequence 7, Application US/08129610
; Patent No. 5436002
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels

; TITLE OF INVENTION: No. 5436002el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,610
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleonensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-08-129-610-7

Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVILTPSSDVVNYSEIQVA----POYVNOALTAKYFQAI-----DGLTLRPFDE 54
Db 38 RVILKLV--KDPIDTTQLLEITEIENPNVYLQALAAAFQDALVPTETFEGEAIRFSMP 95
Qy 55 KALQIANDI-POAAVNTLNQTVQGVSMIDKIVDMKNVLSIVIDNKKFWDQVTA 113
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Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSMIDRVISVLKTMGVALSG-SIITQLTA 154
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Db 155 AITDFTNLNTQKDSAWFMWKGKTSHTQNTYTNVMFAIQNETTGRVMMCVPIGFEIRVFT 214
Qy 174 EKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 6
US-08-129-609A-7
; Sequence 7, Application US/08129609A
; Patent No. 5489432
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: M. Keith Kennedy
; APPLICANT: John Brookes Randall
; APPLICANT: David Orlin Brower
; APPLICANT: H. Ernest Schnepf
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active
; AGAINST Cockroaches and Genes Encoding Cockroach-Active Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,609A
; FILING DATE: 30-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958,551
; FILING DATE: 19-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/788,654
; FILING DATE: 6-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: M/J 101.C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 2017635
US-08-129-609A-7

Query Match 36.4%; Score 423.5; DB 1; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
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Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;
Qy 5 RVITLTPSSDVNYSYIYQVA---POYVNOALTLLAKYFQGA-----DGSTLRPDE 54
Db 38 RVIIYLVK--KDPIDTTLQLEITEIENPNYVLQALQAAAFQDALVPTETFEGEAIRFSMP 95
Qy 55 KALQIANDI--PQAAVAVNTLQTVQVQSVMIKDVIDIMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPKGAVVAYTDQTLQSNNQVSMIDRVISVLKTMGVALSG-SIITQLTA 154
Qy 114 AITNFTNLNQSSEAWIFYKKEDAHKTSYYNIIILFAIQDEBTGVMATLPIAFDISVDI 173
Db 155 AITDFTNLNTQKDSAWFMWKGKTSHTQNTYTNVMFAIQNETTGRVMMCVPIGFEIRVFT 214
Qy 174 EKEKVLFTIKDTENYAVTVKAINVVQALQSSRDSKVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 7
US-08-455-313-7
; Sequence 7, Application US/08455313
; Patent No. 5635480
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: No. 5635480el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,313
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,610
; FILING DATE: 30-SEP-1993
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
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;
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA96.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-08-657-579A-2

Query Match 36.4%; Score 423.5; DB 2; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNAQLTLAKYFQGA1-----DGSTLRFPDFE 54
DB 38 RVIVLKV--KDPIDTTLLEITEIENPNYVLQAIQAAAFQDALVPTETETGEAIRFSMP 95

QY 55 KALQIANDI-POAAVNTLNQTVQGVTSVMKD1KVIDIMKNVLSIVIDNKKTFWDQVTA 113
DB 96 KGLEVAKTQPKGAVVAYTDTLSQNNQVSMIDRVISVLKTVMGVALSG-SIITQLTA 154

QY 114 AITNTFTNLNQSSEAWIFYYKEDAHKTSYYN1LFAIQDEETGGMATLPIAFDISYDI 173
DB 155 AITDTFTNLNTQKDSAWVFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGEIRVFT 214

QY 174 EKEKLVFTTIKDTENYAVTVKAINVVQALQSSRSKVVDD---AFKSPRHL 220
DB 215 DKRTVLFITTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 10
US-09-224-025-7
; Sequence 7, Application US/09224025
; Patent No. 6150165
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: No. 6150165el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,025
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICANT: Jewel Payne
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; APPLICATION NUMBER: 08/455,313
; FILING DATE: 08/093,199
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
; US-09-224-025-7

Query Match 36.4%; Score 423.5; DB 3; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVNAQLTLAKYFQGA1-----DGSTLRFPDFE 54
DB 38 RVIVLKV--KDPIDTTLLEITEIENPNYVLQAIQAAAFQDALVPTETETGEAIRFSMP 95

QY 55 KALQIANDI-POAAVNTLNQTVQGVTSVMKD1KVIDIMKNVLSIVIDNKKTFWDQVTA 113
DB 96 KGLEVAKTQPKGAVVAYTDTLSQNNQVSMIDRVISVLKTVMGVALSG-SIITQLTA 154

QY 114 AITNTFTNLNQSSEAWIFYYKEDAHKTSYYN1LFAIQDEETGGMATLPIAFDISYDI 173
DB 155 AITDTFTNLNTQKDSAWVFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGEIRVFT 214

QY 174 EKEKLVFTTIKDTENYAVTVKAINVVQALQSSRSKVVDD---AFKSPRHL 220
DB 215 DKRTVLFITTKDYANYSVNIQTLRPAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 11
US-09-706-541-7
; Sequence 7, Application US/09706541
; Patent No. 6689743
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
; IMMEDIATE SOURCE:
; LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
; CLONE: 201T635
PCT-US94-07887-7

Query Match 36.4%; Score 423.5; DB 5; Length 265;
Best Local Similarity 40.9%; Pred. No. 3e-35;
Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVILTPSSDVVNYSEIYQVA-----POYVNOALTAKYFQGA-----DGSTLRDFPE 54
Db 38 RVILKV--KPIDTQLLEITEENPNYVLQALAAAFQDALVPTETFEGEAIRFSMP 95

Qy 55 KALQIANDI-POAAVNTLNQTVQSGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTA 113
Db 96 KGLEVAKTIQPKGAVVAYTDTQLSQSNQVSMIDRVISVLKTVNGVALSG-SIITQLTA 154

Qy 114 AITNFTNLNQSSEAWIFYKKEDAHKTSYYNINLFAIQDEETGGVMATLPIAFDISYDI 173
Db 155 AITDFTNLNQTQKSAWVFWGKESHQNTYNNVWFALQNETTGRVMMCVPIGEIRVFT 214

Qy 174 EKEKLVFTIKDTEYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 215 DKRTVLFTTKDYANSVNIQTLRFAQPLIDSRALSINDLSEALRSSKYL 264

RESULT 13
US-08-129-610-8
; Sequence 8, Application US/08129610
; Patent No. 5436002
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: Kenneth Narva
; APPLICANT: Kendrick Akira Uyeda
; APPLICANT: Christine Julie Stalder
; APPLICANT: Tracy Ellis Michaels
; TITLE OF INVENTION: No. 5436002el Bacillus thuringiensis Isolates and Toxins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL USA
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,610
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,199
; FILING DATE: 15-JUL-1993
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,350
; FILING DATE: 17-NOV-1992
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; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/746,751
; FILING DATE: 21-AUG-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/708,266
; FILING DATE: 28-MAY-1991
; NAME:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/647,399
; FILING DATE: 29-JAN-1991
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: MA55CCD.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus thuringiensis
; STRAIN: neoleoensis
; INDIVIDUAL ISOLATE: PS201T6
US-08-129-610-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVNYSIYQVA-POYVNOALTAKYFQGA-----DGSTLRDFPEKALQIANDI-POA 66
Db 6 DTTQLLEITEENPNYVLQALAAAFQDALVPTETFEGEAIRFSMPKGLEVAKTIQPKG 65

Qy 67 AVVNTLNQTVQSGTVQVSMIDKIVDIMKNVLSIVIDNKKFWDQVTAITNFTNLNQS 126
Db 66 AVVAYTDQLSQSNQVSMIDRVISVLKTVNGVALSG-SIITQLTAITDFTNLNQTOK 124

Qy 127 SEAWIFYKKEDAHKTSYYNINLFAIQDEETGGVMATLPIAFDISYDIEKEKLVFTIKDT 186
Db 125 DSAWVFWGKESHQNTYNNVWFALQNETTGRVMMCVPIGEIRVFTDKRTVLPLTTKDY 184

Qy 187 ENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 185 ANYSVNIQTLRFAQPLIDSRALSINDLSEALRSSKYL 221

RESULT 14
US-08-129-609A-8
; Sequence 8, Application US/08129609A
; Patent No. 5489432
; GENERAL INFORMATION:
; APPLICANT: Jewel Payne
; APPLICANT: M. Keith Kennedy
; APPLICANT: John Brookes Randall
; APPLICANT: David Orlin Brower
; APPLICANT: H. Ernest Schnepf
; TITLE OF INVENTION: Bacillus thuringiensis Isolates Active
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
```


STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 30-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/958,551
FILING DATE: 19-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/788,654
FILING DATE: 6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/J 101.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: neoleoensis
INDIVIDUAL ISOLATE: PS201T6
US-08-129-609A-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

QY 15 DVVNYSEIYQVA-POYVNAQALTAKYFOGAI-----DGSTLRPFDFEKALQIANDI-PQA 66
DB 6 DTTQLLEITEIENPNVYLQALAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65
QY 67 AVVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
DB 66 AVVAYTDQTLSSQNNQVSMIDRVISVLKTVMGVALSG-SIITQLTAATDTFTNLNTQK 124
QY 127 SEAWIFYYKEDAHKTSYYNINILFAIQDEBTGGVMATLPIAFDISVDIEKEKLVFTIKDT 186
DB 125 DSAAVFWGKESHQNTYNNVNFALQNETTGRVMMCMVPIGFIRVFTDKRTVFLFTTKDY 184
QY 187 ENYAVTVKAINVQALQSSRDSKVVD---AFKSPRHL 220
DB 185 ANYSVNIQTLRPAQFLIDSRALSINDLSEALRSSKYL 221

RESULT 15
US-08-455-313-8
Sequence 8, Application US/08455313
Patent No. 5635480
GENERAL INFORMATION:
APPLICANT: Jewel Payne
APPLICANT: Kenneth Narva
APPLICANT: Kendrick Akira Uyeda
APPLICANT: Christine Julie Stalder
APPLICANT: Tracy Ellis Michaels
TITLE OF INVENTION: No. 5635480el Bacillus thuringiensis Isolates and Toxins
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSES: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,313
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,610
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 08/093,199
FILING DATE: 15-JUL-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,350
FILING DATE: 17-NOV-1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/746,751
FILING DATE: 21-AUG-1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/708,266
FILING DATE: 28-MAY-1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,399
FILING DATE: 29-JAN-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA55CCD.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: neoleoensis
INDIVIDUAL ISOLATE: PS201T6
US-08-455-313-8

Query Match 35.8%; Score 417; DB 1; Length 222;
Best Local Similarity 41.9%; Pred. No. 1.1e-34;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

QY 15 DVVNYSEIYQVA-POYVNAQALTAKYFOGAI-----DGSTLRPFDFEKALQIANDI-PQA 66
DB 6 DTTQLLEITEIENPNVYLQALAAAFQDALVPTETEFGEAIRFSMPKGLEVAKTIQPKG 65
QY 67 AVVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
DB 66 AVVAYTDQTLSSQNNQVSMIDRVISVLKTVMGVALSG-SIITQLTAATDTFTNLNTQK 124
QY 127 SEAWIFYYKEDAHKTSYYNINILFAIQDEBTGGVMATLPIAFDISVDIEKEKLVFTIKDT 186

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:47:47 ; Search time 174 Seconds
(without alignments)
679.829 Million cell updates/sec

Title: US-10-767-605-2

Perfect score: 1165
Sequence: 1 MFNRVTLTVPSDDVNNYS.....DAFKSPRHLPRKRHKICSNS 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Result No.	Score	Query Match	Length	ID	Description
1	1160	99.6	231	2 Q93M48	Q93M48 bacillus th
2	637	54.7	259	1 CYAA_BACTY	Q04470 bacillus th
3	637	54.7	259	2 Q71KW8	Q71KW8 bacillus th
4	597	51.2	260	2 Q8VNX0	Q8VNX0 bacillus th
5	595	51.1	263	1 CYBA_BACTI	Q45723 bacillus th
6	592.5	50.9	263	1 CYBB_BACTJ	Q32322 bacillus th
7	586	50.3	262	2 Q9L878	Q9L878 bacillus th
8	456	39.1	249	1 CXAA_BACTI	P05069 bacillus th
9	448	38.5	157	2 O52298	O52298 bacillus th
10	448	38.5	157	2 Q7BVD4	Q7BVD4 bacillus th
11	444	38.1	156	2 Q30895	Q30895 bacillus th
12	443	38.0	156	2 Q3R9C0	Q3R9C0 bacillus th
13	442	37.9	156	2 Q30969	Q30969 bacillus th
14	423.5	36.4	265	1 CXBA_BACTW	Q45790 bacillus th
15	416.5	35.8	250	1 CXAB_BACTV	P94594 bacillus th
16	344.5	29.6	525	2 Q8KNJ9	Q8KNJ9 bacillus th
17	151.5	13.0	217	2 Q6USC4	Q6USC4 volvariella
18	105.5	9.1	880	2 Q91R5	Q91R5 clostridium
19	105.5	9.1	1830	2 Q7YYV0	Q7YYV0 cryptospori
20	105.5	9.1	2528	2 Q86J36	Q86J36 dictyosteli
21	103	8.8	477	2 Q68960	Q68960 helicobacte
22	103	8.8	477	2 Q25326	Q25326 helicobacte
23	102.5	8.8	981	2 Q8MET8	Q8MET8 parachlanyd
24	101	8.7	477	2 Q9ZLM7	Q9ZLM7 helicobacte
25	99.5	8.5	4540	1 Y0HC_PARTF	Q27171 paramecium
26	98.5	8.5	201	1 Y007_NPVAC	P24650 autographa
27	97.5	8.4	1442	2 Q83858	Q83858 nilaparvata
28	97	8.3	566	2 Q6CT48	Q6CT48 kluyveromyc
29	96.5	8.3	343	1 HRCA_BACSU	P35499 bacillus su
30	95.5	8.2	421	1 TYPH_MYCGE	P47297 mycoplasma
31	95.5	8.2	1876	2 Q8DQNS	Q8DQNS streptococc

32 95 8.2 1076 1 CARB_BUCBP PS9448 buchnera ap
33 94.5 8.1 249 2 Q9K9Y9 Q9K9Y9 bacillus ha
34 94.5 8.1 393 1 RPN9_YEAST Q04062 saccharomyc
35 94 8.1 498 2 Q7QSH6 Q7QSH6 giardia lam
36 93.5 8.0 660 2 Q81EH1 Q81EH1 bacillus ce
37 93 8.0 773 2 Q8KZM6 Q8KZM6 piscophilus
38 92.5 7.9 1018 2 Q8RFH6 Q8RFH6 fusobacteri
39 92.5 7.9 4688 2 Q9PQ08 Q9PQ08 ureaplasma
40 92 7.9 297 2 Q7RGC0 Q7RGC0 plasmodium
41 92 7.9 297 2 Q7NBJ7 Q7NBJ7 mycoplasma
42 92 7.9 678 2 Q8XIX7 Q8XIX7 clostridium
43 92 7.9 845 2 Q7R8M2 Q7R8M2 plasmodium
44 92 7.9 1147 2 Q6LEZ7 Q6LEZ7 plasmodium
45 92 7.9 4780 2 Q8IE54 Q8IE54 plasmodium

ALIGNMENTS

RESULT 1

Q93M48 ID Q93M48 PRELIMINARY; PRT; 231 AA.
AC Q93M48;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Insecticidal crystal protein CryET29.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Rupar M.J., Donovan W.F., Tan Y., Slaney A.C.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baum J.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030096; AAK50455.1; -.
DR HSSP; Q04470; 1CBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
SQ SEQUENCE 231 AA; 26194 MW; D3734D9E31E44313 CRC64;

Query Match 99.6%; Score 1160; DB 2; Length 231;

Best Local Similarity 99.6%; Pred. No. 7.1e-80;

Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFNRVTLTVPSDDVNNYSIYQVAPQYVNOALTAKYFOGAIKQVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 1 MFNRVTLTVPSDDVNNYSIYQVAPQYVNOALTAKYFOGAIKQVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Qy 61 NDIPQAAVNTLNTQVQGVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNTQVQGVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Qy 121 NLNQSSEAMIFYKEDAHKTSYYNIFALQDEETGGVMTLPFAPDISVDIEKEKVL 180
Db 121 NLNQSSEAMIFYKEDAHKTSYYNIFALQDEETGGVMTLPFAPDISVDIEKEKVL 180
Qy 181 VTIKDTENYAVTVKAINVQALQSSRSKVVDAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKDTENYAVTVKAINVQALQSSRSKVVDAFKSPRHLPRKRHKICSNS 231

RESULT 2

CYAA_BACTY ID CYAA_BACTY STANDARD; PRT; 259 AA.
AC Q04470;


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RESULT 4
Q8VNX0 Q8VNX0 PRELIMINARY; PRT; 260 AA.
ID Q8VNX0 AC Q8VNX0
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cyt2Bc protein.
GN Name=Cyt2Bc;
OS Bacillus thuringiensis (subsp. medellin).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=79672;
RN [1]

SEQUENCE FROM N.A.
RP MEDLINE=21861241; PubMed=11872472;
RX DOI=10.1128/AEM.68.3.1228-1231.2002;
RA Juarez-Perez V., Guerchicoff A., Rubinstein C., Delecluse A.;
RT "Characterization of Cyt2Bc toxin from Bacillus thuringiensis subsp. medellin.";
RL Appl. Environ. Microbiol. 68:1228-1231(2002).
DR EMBL; AJ251979; CAC80987.1; -.
DR HSP; Q04470; ICBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin CytB; 1.
SQ SEQUENCE 260 AA; 29716 MW; 8B87917B6FB485B4 CRC64;

Query Match 51.2%; Score 597; DB 2; Length 260;
Best Local Similarity 52.9%; Pred. No. 3e-37;
Matches 120; Conservative 43; Mismatches 62; Indels 2; Gaps 2;

QY 5 RVITLTVPSSDVVNYSEIQVAPQVYVQALTLAKYFQGAIDGSTLRDFEPEKALQIANDIP 64
DB 27 RHIALTVPESSDITNFNEIFYVEPQYIAQRLTNTFQGAIDPTLTLNFPEKALQIANGLP 86
QY 65 QAAVNTLNQTVQOQTGVQSVNMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFTNLNS 124
DB 87 NAGVTGTLNQSVTHQTIETSVMSIQKEIIRSVGLVINSANFNWVNSAINTFTNLPEP 146
QY 125 QSEAWIFYKEDAKHTSYNYNLPFAIQDEETGGVWATLPIDAFSDVIEKSKVLFTVIK 184
DB 147 QVDENWIVRNLSANQTSYYKILFSIQNEDTGRFMAVLPIAFETVDVKQQLLFTIK 206
QY 185 DTENYAVTVKAINVQALQSSRDSKVDAFKSPRH-LPRKRHKICSN 230
DB 207 DSARYEVKMKALTVVQAL-DSYNAPIIDVFNHNSLHRPNYHILQN 252

RESULT 5
CYBA_BACTI
ID CYBA_BACTI STANDARD; PRT; 263 AA.
AC Q45723;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-28a cytolytic delta-endotoxin (29 kDa cytolytic toxin).
GN Name=Cyt2Bai; Synonyms=Cyt2Ba7, CytB;
OS Bacillus thuringiensis (subsp. israelensis).
OC Plasmid pRX80.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430;
RN [1]

SEQUENCE FROM N.A.
RP STRAIN=4Q2;
RX MEDLINE=97355937; PubMed=9212418;
RA Guerchicoff A., Ugalde R.A., Rubinstein C.P.;
RT "Identification and characterization of a previously undescribed cyt gene in Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 63:2716-2721(1997).
CC the epithelial cell membrane of the insect midgut (By similarity).

RESULT 6
CYBB_BACTJ
ID CYBB_BACTJ STANDARD; PRT; 263 AA.
AC O32322;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-2Bb cytolytic delta-endotoxin (30 kDa cytolytic toxin).
GN Name=Cyt2Bbi;
OS Bacillus thuringiensis (subsp. jegasethan).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=56955;
RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=97394951; PubMed=9251213;
RX Cheong H., Gill S.S.;
RT "Cloning and characterization of a cytolytic and mosquitoicidal delta-endotoxin from Bacillus thuringiensis subsp. jegasethan.";
RL Appl. Environ. Microbiol. 63:3254-3260(1997).
CC the epithelial cell membrane of the insect midgut (By similarity).

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CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- PM: Active after proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U82519; AAB93477.1; -.
DR HSSP; Q04470; 1CBY.
DR InterPro; IPR001615; Endotoxin CytB.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin CytB; 1.
KW Direct protein sequencing; Sporulation; Toxin.
SQ SEQUENCE 263 AA; 30059 MW; BDB7B72CDE090D9D CRC64;

Query Match 50.9%; Score 592.5; DB 1; Length 263;
Best Local Similarity 55.2%; Pred. No. 6.7e-37;
Matches 116; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

QY 5 RVILTVSPSSDVNVSEIYQVAPQVVAQALTLAKYFQGAIDGSTLRDPFEKALQIANDIP 64
DB 27 RHILTVSPSSDIAGSFEIYFLEPQVVAQALRLTNTFQAIDPLTLNFEKALQIANGLP 86
QY 65 QAAVNTLNQVTVQGVSVMDIKVIDMKNVLSIVDNKKFWDQVTAATNTFTNLNS 124
DB 87 NAGTGTNLNQSVIQOTIISVMSIQKEIIRSVGLVINSANFVNSVVAITNTFTNLEP 146
QY 125 QESAWIFYYKEDAHKTSYYNIIFAIQDEBTGGVMATLPFAFISVDIEKEKVLFTVIK 184
DB 147 QVDENWIWNRNLSATHTSYFYKILFSIQNEDTGAFMAVLPIAFETVDVQKQLFIIR 206
QY 185 DTENYAVTVKAINVVOALQSSRDSKVVDAP 214
DB 207 DSARYEVKMKALTVVQQL-DSYNAPIIDVF 235

RESULT 7
Q9L878 PRELIMINARY; PRT; 263 AA.
AC Q9L878;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytolytic toxin Cyt2Ba8.
GN Name=cyt2Ba8;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T36;
RA Yu J., Pang Y.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF215646; AAF37223.1; -.
DR HSSP; Q04470; 1CBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin CytB.
DR Pfam; PF01338; Bac thur toxin; 1.
DR ProDom; PD009844; Endotoxin CytB; 1.
SQ SEQUENCE 263 AA; 29895 MW; 2DFD3466049C5B9D CRC64;

Query Match 50.3%; Score 586; DB 2; Length 263;
Best Local Similarity 52.0%; Pred. No. 2.1e-36;
Matches 118; Conservative 44; Mismatches 63; Indels 2; Gaps 2;

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QY 5 RVILTVSPSSDVNVSEIYQVAPQVVAQALTLAKYFQGAIDGSTLRDPFEKALQIANDIP 64
DB 30 RHILTVSPSSDITNFNEIYFVEPQYIAQALRLTNTFQAIDPLTLNFEKALQIANGLP 89
QY 65 QAAVNTLNQVTVQGVSVMDIKVIDMKNVLSIVDNKKFWDQVTAATNTFTNLNS 124
DB 90 NAGTGTIIQSVIHQTIETVSVMSIQKEIIRSVGLVINSANFVNSVVAITNTFTNLEP 149
QY 125 QESAWIFYYKEDAHKTSYYNIIFAIQDEBTGGVMATLPFAFISVDIEKEKVLFTVIK 184
DB 150 QVDENWIWNRNLSATHTSYFYKILFSIQNEDTGAFMAVLPIAFETVDVQKQLFIIR 209
QY 185 DTENYAVTVKAINVVOALQSSRDSKVVDAPFSPH-LPRKHKICSN 230
DB 210 DSARYEVKMKALTVVQAL-DSYNAPIIDVFVNRVNSLHRPNHNLQN 255

RESULT 8
CXAA_BACTI STANDARD; PRT; 249 AA.
ID_CXAA_BACTI
AC P05069; P05628;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Type-1Aa cytolytic delta-endotoxin (27 kDa cytolytic toxin).
GN Name=cyt1Aa; Synonyms=cytA;
OS Bacillus thuringiensis (subsp. israelensis), and
OC Bacillus thuringiensis (subsp. morrisoni).
OG Plasmid 72 Kb.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1430, 1441;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=87086764; PubMed=3025452;
RA Ward E.S., Ellar D.J.;
RT "Bacillus thuringiensis var. israelensis delta-endotoxin. Nucleotide
RT sequence and characterization of the transcripts in Bacillus
RT thuringiensis and Escherichia coli.";
RL J. Mol. Biol. 191:1-11(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=87086767; PubMed=3025453;
RA Ward E.S., Ridley A.R., Ellar D.J., Todd J.A.;
RT "Bacillus thuringiensis var. israelensis delta-endotoxin. Cloning and
RT expression of the toxin in sporogenic and asporogenic strains of
RT Bacillus subtilis.";
RL J. Mol. Biol. 191:13-22(1986).
RN [3]
RP SEQUENCE FROM N.A., AND MUTAGENESIS.
RC SPECIES=B.t.israelensis;
RX MEDLINE=89011977; PubMed=2845100;
RA Ward E.S., Ellar D.J., Chilcott C.N.;
RT "Single amino acid changes in the Bacillus thuringiensis var.
RT israelensis delta-endotoxin affect the toxicity and expression of the
RT protein.";
RL J. Mol. Biol. 202:527-535(1988).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.israelensis;
RX MEDLINE=86067227; PubMed=4070003;
RA Waalwijk C., Duilemans A.M., van Worum M.E.S., Visser B.;
RT "Molecular cloning and the nucleotide sequence of the Mr 28 000
RT crystal protein gene of Bacillus thuringiensis subsp. israelensis.";
RL Nucleic Acids Res. 13:8207-8217(1985).
RN [5]
RP REVISIONS TO 34-35.
RC SPECIES=B.t.israelensis;
RA Waalwijk C.;
RL Submitted (FEB-1986) to the EMBL/GenBank/DBJ databases.
RN [6]

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RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morriisoni; STRAIN=PG14;
RX MEDLINE=87203386; PubMed=3575104;
RA Earp D.J., Ellar D.J.;
RT "Bacillus thuringiensis var. morriisoni strain PG14: nucleotide
RL sequence of a gene encoding a 27kDa crystal protein.";
RN Nucleic Acids Res. 15:3619-3619(1987).

[7]
RP SEQUENCE FROM N.A.
RC SPECIES=B.t.morriisoni; STRAIN=PG14;
RA Galfart N.J., Sivasubramanian N., Federici B.A.;
RT "Plasmid location, cloning, and sequence analysis of the gene encoding
RT a 27.3-kilodalton cytolytic protein from Bacillus thuringiensis subsp.
RT morriisoni (PG-14).";
RL Curr. Microbiol. 16:171-177(1987).

CC -!- FUNCTION: Kills the larvae of dipteran insects by making pores in
CC the epithelial cell membrane of the insect midgut. Acts on
CC mosquitoes and black flies.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -!- PTM: Active after proteolytic processing.
CC -!- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X04338; CAA27868.1; -
DR EMBL; X03182; CAA26943.1; -
DR EMBL; Y00135; CAA68329.1; -
DR EMBL; M35968; AAR22553.1; -
DR PIR; A24044; A24044.
DR PIR; A27520; A27520.
DR HSSP; Q04470; 1CBY.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac_thur_toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
KW Flaemid; Sporulation; Toxin.
FT VARIANT 82
FT SEQUENCE 249 AA; 27341 MW; E661946298D3989A CRC64;

Query Match 39.1%; Score 456; DB 1; Length 249;
Best Local Similarity 45.6%; Pred. No. 1.3e-26;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;

QY 5 RVITLTVPSS-SDVNVSEIYQV-APQVYNQALTLAKYFQGAIF-----DGSTLRDFEFA 56
DB 25 RVITLRVEDPNEINLLSNEIDNPYILQAIMLANAFQNALVPTSTDFGDLRFSPK 84

QY 57 LOIANDI-PQAAVNTLQVQVGVQVSVIMDKIVDMKNVLSIVDKKPFWDQVTA 115
DB 85 LEIANTITPAGVAVSYVDQVNTQNNQSVIMDKIVDMKNVLSIVDKKPFWDQVTA 143

QY 116 TMTFTNLNSQSEAWIFYKKDAHTSYNNILFAIQDEETGGVWATLPIAFDISVDIEK 175
DB 144 TMTFTNLNTQKNEAWIFWKGATNTNTYNNVLFQAIQNAQVGVVCPVGFVKVSAVK 203

QY 176 EKVLFVTIKDTENTAVTVAKNVNVQALQSSRDSKVVD 212
DB 204 EQVLFVTIKDQSNVNVNQLKFAQLVSSSQYPIAD 240

RESULT 9
O52298 PRELIMINARY; PRT; 157 AA.
AC O52298;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytolytic toxin (Fragment).
GN Name=Cyt2Ba;
OS Bacillus thuringiensis (subsp. tenebrionis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1444;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97355937; PubMed=9212418;
RA Guerschicoff A., Ugalde R.A., Rubinstein C.P.;
RT "Identification and characterization of a previously undescribed cyt
RT gene in Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 63:2716-2721(1997).
DR EMBL; AF034926; AAB95384.1; -
DR HSSP; Q04470; 1CBY.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac_thur_toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
FT NON_TER 1
FT NON_TER 157
FT SEQUENCE 157 AA; 17716 MW; 7A00550DD3E8A124 CRC64;

Query Match 38.5%; Score 448; DB 2; Length 157;
Best Local Similarity 55.5%; Pred. No. 3e-26;
Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;

QY 40 FQAGIDGSLRPFDFKALQIANDIPQAAVNTLQVQVGVQVSVIMDKIVDMKNVLS 99
DB 3 FQAGIDPLTNFNFKEKALQIANGLENAGVTGTINQSVIHQTIIEVSMISQIKIIRSVL 62

QY 100 IVIDNKKFWDQVTAITMTFTNLNSQSEAWIFYKKDAHTSYNNILFAIQDEETGGV 159
DB 63 LVINSANFNWSVSAITMTFTNLNSQSEAWIFYKKDAHTSYNNILFAIQDEETGGV 122

QY 160 MATLPIAFDISVDIEKVKLVFVTIKDTENTAVTVA 194
DB 123 MAILPIAFETVQVQKQLLFTTIKDSARYEVGMK 157

RESULT 10
Q7BVD4
ID Q7BVD4 PRELIMINARY; PRT; 157 AA.
AC Q7BVD4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative cytolytic toxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=4K3;
RA MEDLINE=97355937; PubMed=9212418;
RA Guerschicoff A., Ugalde R.A., Rubinstein C.P.;
RT "Identification and characterization of a previously undescribed cyt
RT gene in Bacillus thuringiensis subsp. israelensis.";
RL Appl. Environ. Microbiol. 63:2716-2721(1997).
DR EMBL; AF022886; AAB87600.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR InterPro; IPR001615; Endotoxin_CytB.
DR Pfam; PF01338; Bac_thur_toxin; 1.
DR ProDom; PD009844; Endotoxin_CytB; 1.
FT NON_TER 1
FT NON_TER 157
FT SEQUENCE 157 AA; 17716 MW; 7A00550DD3E8A124 CRC64;

Query Match 38.5%; Score 448; DB 2; Length 157;
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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:59:48 ; Search time 159 Seconds
(without alignments)
558.683 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFNVRVITLTPSSDVVNVYS.....DAFKSPRLPRKHKICNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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 - 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1165	100.0	231	14 US-10-386-972-2	Sequence 2, Appli
2	1165	100.0	231	16 US-10-767-605-2	Sequence 2, Appli
3	101	8.7	477	15 US-10-335-977-9400	Sequence 9400, Ap
4	97	8.3	1833	8 US-08-945-567D-4	Sequence 4, Appli
5	97	8.3	1833	8 US-08-621-944A-4	Sequence 4, Appli
6	97	8.3	1833	14 US-10-175-282-4	Sequence 4, Appli
7	97	8.3	1833	14 US-10-175-275-4	Sequence 4, Appli
8	97	8.3	1992	8 US-08-945-567D-3	Sequence 3, Appli
9	97	8.3	1992	8 US-08-621-944A-3	Sequence 3, Appli
10	97	8.3	1992	14 US-10-175-282-3	Sequence 3, Appli
11	97	8.3	1992	14 US-10-175-275-3	Sequence 3, Appli

12	95.5	8.2	421	15	US-10-282-122A-63417	Sequence 63417, A
13	95.5	8.2	1876	15	US-10-282-122A-73861	Sequence 73861, A
14	94.5	8.1	249	15	US-10-369-493-17326	Sequence 17326, A
15	94.5	8.1	356	15	US-10-424-599-217207	Sequence 217207, A
16	94	8.1	372	15	US-10-425-114-53891	Sequence 53891, A
17	94	8.1	383	15	US-10-425-114-59141	Sequence 59141, A
18	93	8.0	2122	9	US-09-813-214A-9	Sequence 9, Appli
19	92.5	7.9	4688	15	US-10-282-122A-76865	Sequence 76865, A
20	90	7.7	1280	15	US-10-452-024-139	Sequence 139, App
21	90	7.7	1280	15	US-10-452-024-140	Sequence 140, App
22	89.5	7.7	1278	15	US-10-452-024-152	Sequence 152, App
23	89.5	7.7	1278	15	US-10-205-516-12	Sequence 12, Appl
24	89.5	7.7	1288	15	US-10-205-516-26	Sequence 26, Appl
25	89.5	7.7	4961	14	US-10-114-153-64	Sequence 64, Appl
26	89	7.6	246	15	US-10-282-122A-53616	Sequence 53616, A
27	89	7.6	1101	16	US-10-437-963-172676	Sequence 172676, A
28	89	7.6	1389	17	US-10-732-923-17027	Sequence 17027, A
29	89	7.6	1805	10	US-09-820-843A-73	Sequence 73, Appl
30	89	7.6	1805	15	US-10-282-122A-63513	Sequence 63513, A
31	89	7.6	1805	17	US-10-732-923-3303	Sequence 3303, Ap
32	88.5	7.6	736	15	US-10-282-122A-72461	Sequence 72461, A
33	88	7.6	736	15	US-10-387-977-105	Sequence 105, App
34	87.5	7.5	935	16	US-10-478-451-7	Sequence 7, Appli
35	87.5	7.5	1087	17	US-10-732-923-8260	Sequence 8260, Ap
36	87	7.5	653	9	US-09-759-010-2	Sequence 2, Appli
37	87	7.5	653	16	US-10-408-765A-13	Sequence 13, Appl
38	87	7.5	911	14	US-10-032-585-7655	Sequence 7655, Ap
39	87	7.5	1170	16	US-10-437-963-107142	Sequence 107142, A
40	86.5	7.4	311	17	US-10-732-923-19018	Sequence 19018, A
41	86.5	7.4	474	14	US-10-127-032-100	Sequence 100, App
42	86.5	7.4	1300	9	US-09-815-242-4903	Sequence 4903, Ap
43	86.5	7.4	1300	9	US-09-815-242-10906	Sequence 10906, A
44	86.5	7.4	1418	15	US-10-369-493-22315	Sequence 22315, A
45	86.5	7.4	1903	17	US-10-766-993-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-386-972-2
; Sequence 2, Application US/10386972
; Publication NO. US20030167521A1
; GENERAL INFORMATION:
; APPLICANT: Rupa, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: Bacillus thuringiensis CryET29 Compositions Toxic to Coleopteran
; FILE REFERENCE: MECO:017--2
; CURRENT APPLICATION NUMBER: US/10/386,972
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-386-972-2

Query Match 100.0%; Score 1165; DB 14; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFNVRVITLTPSSDVVNVSEIYVAPQVNVNALTAKYFOGAIIDGTLRFDFEKALQIA 60
DB 1 MFNVRVITLTPSSDVVNVSEIYVAPQVNVNALTAKYFOGAIIDGTLRFDFEKALQIA 60

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QY 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
QY 121 NLNSQSEAWIFYYKEDAHKTSYYNIIILFAIQDEETGGVMTPLPIAFDISVDIEKEKVL 180
Db 121 NLNSQSEAWIFYYKEDAHKTSYYNIIILFAIQDEETGGVMTPLPIAFDISVDIEKEKVL 180
QY 181 VTIKOTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKOTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
```

RESULT 2

```
US-10-767-605-2
; Sequence 2, Application US/10767605
; Publication No. US20040127695A1
; GENERAL INFORMATION:
; APPLICANT: Rutar, Mark J.
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Slaney, Annette C.
; TITLE OF INVENTION: Plants Toxic to Coleopteran Insects and Ctenocephalides Spp.
; TITLE OF INVENTION: (Amended)
; FILE REFERENCE: MECO-017--3
; CURRENT APPLICATION NUMBER: US/10/767,605
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 10/386,972
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: 09/611,216
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 08/721,259
; PRIOR FILING DATE: 1996-09-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; TYPE: PR1
; ORGANISM: Bacillus thuringiensis
US-10-767-605-2
```

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Query Match 100.0%; Score 1165; DB 16; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MFFNRVITLTVPSDDVNVSEIYQVAPQVNVQALTLAKYFQGAIDGSTLRDFEKAQIA 60
Db 1 MFFNRVITLTVPSDDVNVSEIYQVAPQVNVQALTLAKYFQGAIDGSTLRDFEKAQIA 60
QY 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
Db 61 NDIPQAAVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQVTAATNTFT 120
QY 121 NLNSQSEAWIFYYKEDAHKTSYYNIIILFAIQDEETGGVMTPLPIAFDISVDIEKEKVL 180
Db 121 NLNSQSEAWIFYYKEDAHKTSYYNIIILFAIQDEETGGVMTPLPIAFDISVDIEKEKVL 180
QY 181 VTIKOTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
Db 181 VTIKOTENYAVTVKAINVQALQSSRDSKVVDFAFKSPRHLPRKRHKICSNS 231
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RESULT 3

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US-10-335-977-9400
; Sequence 4, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9400:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...477
; SEQUENCE DESCRIPTION: SEQ ID NO: 9400:
US-10-335-977-9400
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Query Match 8.7%; Score 101; DB 15; Length 477;
Best Local Similarity 20.1%; Pred. No. 1.4;
Matches 46; Conservative 55; Mismatches 90; Indels 38; Gaps 10;
QY 2 PFN---RVITLTVP-----SSDVNVSEIYQVAPQVNVQALTLAKYFQGAIA---DGSTLR 51
Db 199 YFNLMARIALQKLEQIQTDIKRVTKLYDKGLTTDIDQLSKA--QGNLSEYDILDMQF 256
QY 52 DFEKALQIANDIPQAAVNVNTLNQTVQGGTVQVSMIDKIVDMKNVLSIVIDNKKFWDQV 111
Db 257 ALEQNRLTLEVTNLNVKLNKKTITIDAPNLQRLREQD-LVSLREQISALRYQNKQL---- 311
QY 112 TAAITNTFTNLNSQSEAWIFYYKEDAHKTSYYNIIILFAIQDEETGGVMTPLPIAFDISV 171
Db 312 ----NYPKIDVDFS--WLEWIKPAYATGRFGN--FVPGQQTAGTATATLNIFDDIGL 362
QY 172 DIEKEKVLFTIKOTENYA-----VTVKAINVQVQ-LQSSRDS 208
Db 363 SLQKQSIMLQGLANEKNLAYKKLEQKDEQLYRKSLDITARAKIESKAS 411
```

RESULT 4

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US-08-945-567D-4
; Sequence 4, Application US/08945567D
; Publication No. US20010014672A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; TITLE OF INVENTION: MORAXELLA
; FILE REFERENCE: 1038-745 MIS
```

```
; CURRENT APPLICATION NUMBER: US/08/945,567D
; CURRENT FILING DATE: 1996-04-29
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-08-945-567D-4

Query Match      8.3%; Score 97; DB 8; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
DB 898 SHDVTGKGIYDLKTELENKISSHTAKQNSLHEFSVADEQGNFTVSNPYSSYDTSKTS 957
QY 62 DIPQAAVNTLNQTVQOQGTQVQSVNMIDKIVDIMK-----NVLISVIDNKKFMDQVTAI 115
DB 958 DVIITFAGENGITTKVNGVVRGIDQTKGLTTPKLTGVNNGKGIVDSQNGQNTIT-GL 1016
QY 116 TWTFTNLNSQSEAWIFYKEDAHKTSYYNLFIAQDEE---TGGVMATLPIAFDISVD 172
DB 1017 SNTLANVTNDKGSV-----RTTEQGNI---IKDEDKTRAASIVDVLVSAGFNLOQN 1063
QY 173 IEKEKVLFTIKDTENYAVTVKAINVQALQSSRDSKV 211
DB 1064 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1100

RESULT 5
US-08-621-944A-4
; Sequence 4, Application US/08621944A
; Publication No. US2002068070A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
; TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,944A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,370
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I

; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-587
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-621-944A-4

Query Match      8.3%; Score 97; DB 8; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
DB 898 SHDVTGKGIYDLKTELENKISSHTAKQNSLHEFSVADEQGNFTVSNPYSSYDTSKTS 957
QY 62 DIPQAAVNTLNQTVQOQGTQVQSVNMIDKIVDIMK-----NVLISVIDNKKFMDQVTAI 115
DB 958 DVIITFAGENGITTKVNGVVRGIDQTKGLTTPKLTGVNNGKGIVDSQNGQNTIT-GL 1016
QY 116 TWTFTNLNSQSEAWIFYKEDAHKTSYYNLFIAQDEE---TGGVMATLPIAFDISVD 172
DB 1017 SNTLANVTNDKGSV-----RTTEQGNI---IKDEDKTRAASIVDVLVSAGFNLOQN 1063
QY 173 IEKEKVLFTIKDTENYAVTVKAINVQALQSSRDSKV 211
DB 1064 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1100

RESULT 6
US-10-175-282-4
; Sequence 4, Application US/10175282
; Publication No. US20030170657A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; TITLE OF INVENTION: MORAXELLA
; FILE REFERENCE: 1038-1234 MIS
; CURRENT APPLICATION NUMBER: US/10/175,282
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 08/945,567
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-175-282-4

Query Match      8.3%; Score 97; DB 14; Length 1833;
Best Local Similarity 22.8%; Pred. No. 20;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNVSEIYQVAPQYVNVQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
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[illegible]

```

RESULT 7
US-10-175-275-4
; Sequence 4, Application US/10175275
; Publication No. US20030171254A1
; GENERAL INFORMATION:
; APPLICANT: SASAKI, Ken
; APPLICANT: HARKNESS, Robin E.
; APPLICANT: LOOSMORE, Sheena M.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
; FILE REFERENCE: 1038-1235 MIS
; CURRENT APPLICATION NUMBER: US/10/175,275
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 08/945,567
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/431,718
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: 08/478,370
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/621,944
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: PCT/CA96/00264
; PRIOR FILING DATE: 1996-04-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 1833
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-175-275-4

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RESULT 8
US-08-945-567D-3
; Sequence 3, Application US/08945567D
: Publication No. US20010014672A1

```

/ GENERAL INFORMATION:
/ APPLICANT: SASAKI, Ken
/ APPLICANT: HARKNESS, Robin E.
/ APPLICANT: LOOSMORE, Sheena M.
/ APPLICANT: CHONG, Pele
/ APPLICANT: KLEIN, Michel H.
/ TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF MORAXELLA
/ FILE REFERENCE: 1038-745 MIS
/ CURRENT APPLICATION NUMBER: US/08/945,567D
/ CURRENT FILING DATE: 1996-04-29
/ PRIOR APPLICATION NUMBER: 08/431,718
/ PRIOR FILING DATE: 1995-05-01
/ PRIOR APPLICATION NUMBER: 08/478,370
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/621,944
/ PRIOR FILING DATE: 1996-03-26
/ PRIOR APPLICATION NUMBER: PCT/CA96/00264
/ PRIOR FILING DATE: 1996-04-29
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 1992
/ TYPE: PRT
/ ORGANISM: Moraxella catarrhalis
US-08-945-567D-3

Query Match      8.3%; Score 97; DB 8; Length 1992;
Best Local Similarity 22.8%; Pred.No.23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

QY 13 SSDVNNYSIYVAPQYVNVQALTLAKYFQGAIDGSLRDFEFKALQIAN----- 61
DB 1057 SHDVAVTGGKIYDLKTELENKISSTAKTAQNSLHEFSVADEQGNFTVSNPYSSYDTSKTS 1116

QY 62 DIPQAAVNTLNQTVQOGTVQSVSMIDKIVDIMK-----NVLISVIDNKKFWQDVTAAL 115
DB 1117 DVIITFAGENGITTKVNGKVVVRGVIDQTKGLITPKLTGVGNNGKGIVIDSQNGQNTIT-GL 1175

QY 116 TWTFNTNLNQSSEAWIFYFKEDAHKTSYYNYNLFALQDEE---TGGVMTALPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEGNI---IKDEDKTRAASIVDVLSSAGFNLOQN 1222

QY 173 IEKEKLVFTIADTNYAVTVKAINVVQALQSRDSKVV 211
DB 1223 --GEAVDFVSTVDTYNFADGNATTAKTYDDTISKTSKVV 1259

RESULT 9
US-08-621-944A-3
/ Sequence 3, Application US/08621944A
/ Publication No. US20020068070A1
/ GENERAL INFORMATION:
/ APPLICANT: SASAKI, Ken
/ APPLICANT: HARKNESS, Robin E.
/ APPLICANT: LOOSMORE, Sheena M.
/ APPLICANT: KLEIN, Michel H.
/ TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
/ TITLE OF INVENTION: MEMBRANE PROTEIN OF MORAXELLA
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSES: Sim & McBurney
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/621,944A
FILING DATE: 26-MAR-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,370
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-587
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1992 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-621-944A-3

Query Match 8.3%; Score 97; DB 8; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQVYNQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDMK-----NVLSTVDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKKDAHKTSYYNLFALQDEE---TGGVWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222
QY 173 IEKEKLVFTIKDTENYAVTVKAINVQALQSSRDSKV 211
DB 1223 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1259

RESULT 10
US-10-175-282-3
Sequence 3, Application US/10175282
Publication No. US20030170657A1
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
FILE REFERENCE: 1038-1234 MIS
CURRENT APPLICATION NUMBER: US/10/175,282
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 08/945,567
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT

ORGANISM: Moraxella catarrhalis
US-10-175-282-3
Query Match 8.3%; Score 97; DB 14; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQVYNQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDMK-----NVLSTVDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKKDAHKTSYYNLFALQDEE---TGGVWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222
QY 173 IEKEKLVFTIKDTENYAVTVKAINVQALQSSRDSKV 211
DB 1223 --GEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKV 1259

RESULT 11
US-10-175-275-3
Sequence 3, Application US/10175275
Publication No. US20030171254A1
GENERAL INFORMATION:
APPLICANT: SASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
FILE REFERENCE: 1038-1235 MIS
CURRENT APPLICATION NUMBER: US/10/175,275
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 08/945,567
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/431,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-10-175-275-3

Query Match 8.3%; Score 97; DB 14; Length 1992;
Best Local Similarity 22.8%; Pred. No. 23;
Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
QY 13 SSDVNNYSIYQVAPQVYNQALTLAKYFQGAIDGSLRDFEKAQIAN-----61
DB 1057 SHDAVTGGKIYDLKTELENKISSAKTQNSLHFSVADEQGNFTVSNPYSSYDTSKTS 1116
QY 62 DIPQAAVNTLNQTVQOQTVQVSMIDKIVDMK-----NVLSTVDNKKFWDQVTAI 115
DB 1117 DVITFAGENGITTKVNGVVRVIGIDQTKGLTPKLTGVNNGKGVIVDSQNGQNTIT-GL 1175
QY 116 TMTFTNLNSQSEAWIFYKKDAHKTSYYNLFALQDEE---TGGVWATLPIAFDISVD 172
DB 1176 SNTLANVTNDKGSV-----RTTEQGNI---IKDEKTRAASIVDVLVSAGFNLOGN 1222


```

QY 41 --QQADGSLT-----RDFEAAQLANDIPQRAVVNINLQVQQGVVVSVWLDKLVULM 394
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 134 AAEEAQAATILMARRAPPDASSLOEQANKILGNMLWTANHHMQ--YSESCVIDDILD- 190
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 95 KNVLISVIDNKKFKWDQV-TIAIT-----NTFTNLNSQESE-----AWIFYFYKEDA- 138
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 191 --GCSVGISTRYLADKPPTAKVTGFEMSSYFVAWNQOQERAMPKRPFIKWIHANGEDTV 248
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 139 --HKTSYVYNILFAIQDBET-----GGVMATLPIDAFDISVDIEKEKVLF 180
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 249 LPSKSFDLVSIAFLVHECPFTVINLVREAFRLLRPGGTALTDLSLKSKVLQELSPVL 308
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 181 VTIKDENTAYTVKAINVUQALQSRSKDVDAFKSPPHL 220
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 309 TLVKSTPFDDEYYLTDMDETLEAGFVNITSILTDPRH 348
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

[illegible]

Search completed: June 26, 2005, 16:09:50
Job time : 160 secs

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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:47:02 ; Search time 162 Seconds
(without alignments)
551.492 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFNVRVITLTPSSDVVNS.....DAFKSPRHLPRKRHKICSNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1151	98.8	231	2 AAW55027	Bacillus
2	457	39.2	249	2 AAR10282	Mutant 27
3	456	39.1	249	2 AAR04831	Bacillus
4	451	38.7	249	2 AAR10853	Mutant 27
5	450	38.6	249	2 AAR10283	XX
6	450	38.6	249	2 AAR10309	Mutant 27
7	442.5	38.0	220	2 AAR24023	Anticance
8	424	36.4	218	1 AAP90062	XX
9	423.5	36.4	265	2 AAR70754	Delta-end
10	423.5	36.4	265	2 AAR91966	PS201T6 3
11	423.5	36.4	265	2 AAW07850	Delta-end
12	423.5	36.4	265	2 AAY01207	B. thurin
13	417	35.8	222	2 AAR70755	Delta-end
14	417	35.8	222	2 AAR91967	Truncated
15	417	35.8	222	2 AAY01208	B. thurin
16	415.5	35.7	265	3 AAB03646	Cytc toxin
17	103	8.8	401	5 ABUS1322	Helicobac
18	103	8.8	415	5 ABUS2179	Helicobac
19	101	8.7	477	2 AAY10993	H. pylori
20	100	8.6	210	5 ABUS1679	Helicobac
21	97	8.3	1992	4 AAW04505	Moraxella
22	97	8.3	1992	4 AAB69137	M. catarr
23	97	8.3	1992	4 AAB69133	M. catarr
24	97	8.3	2047	4 AAB69134	M. catarr
25	96.5	8.3	201	4 AAB59843	AcMNPV OR

26	95.5	8.2	421	6	ABU35493	Abu35493 Protein e
27	95.5	8.2	1876	6	ABU45937	Abu45937 Protein e
28	94.5	8.1	249	8	ADS28293	Ades28293 Bacterial
29	94.5	8.1	393	6	ABR53069	AbR53069 Protein s
30	94.5	8.1	393	7	ADK62078	Adk62078 Disease t
31	93	8.0	2122	6	ABU08784	Abu08784 Moraxella
32	93	8.0	2123	4	AAE00701	Aae00701 Moraxella
33	92.5	7.9	192	5	ABU51662	Abu51662 Helicobac
34	92.5	7.9	4688	6	ABU48941	Abu48941 Protein e
35	92	7.9	2053	4	AAB69135	Aab69135 M. catarr
36	90	7.7	293	6	ABM73470	Abm73470 Staphyloc
37	89.5	7.7	1059	3	AAU93309	Aay93309 A mangane
38	89.5	7.7	1084	3	AAU93312	Aay93312 A mangane
39	89.5	7.7	4903	6	ABU12072	Abu12072 Human NOV
40	89.5	7.7	4913	8	ADH72246	Adh72246 Human pro
41	89.5	7.7	4961	8	ADH72236	Adh72236 Human pro
42	89	7.6	157	5	ABU50735	Abu50735 Helicobac
43	89	7.6	182	5	ABU52262	Abu52262 Helicobac
44	89	7.6	246	6	ABU25692	Abu25692 Protein e
45	89	7.6	373	7	ADF07179	Adf07179 Bacterial

ALIGNMENTS

RESULT 1
AAW55027
ID AAW55027 standard; protein; 231 AA.
AC AAW55027;
XX
DT 16-SEP-1998 (first entry)
XX
DE Bacillus thuringiensis CryET29 protein.
XX
KW Bacillus thuringiensis; CryET29; crystal protein; Japanese beetle;
KW Southern corn rootworm; Western corn rootworm; Colorado potato beetle;
KW red flour beetle; cat flea; transgenic plant; insecticide.
XX
OS Bacillus thuringiensis.
XX
PN WO9813497-Al.
XX
PD 02-APR-1998.
XX
PF 25-SEP-1997; 97WO-US017507.
XX
PR 26-SEP-1996; 96US-00721259.
XX (ECOG-) ECOGEN INC.
Rupar MJ, Donovan WP, Tan Y, Slaney AC;
WPI; 1998-230707/20.
N-PSDB; AAV27172.
New Bacillus thuringiensis CryET29 crystal protein - having activity against e.g. Southern corn rootworm, Colorado potato beetle, Japanese beetle, red flour beetle and cat fleas.
Claim 2; Fig 1; 101pp; English.
The CryET29 crystal protein has activity against the Southern corn rootworm, Western corn rootworm, Colorado potato beetle, Japanese beetle and red flour beetle and also against fleas, in particular larvae of the cat flea, Ctenocephalides felis. CryET29 can therefore be used to prevent infestations by these insects. The gene can be used to produce transgenic plants which express the toxic proteins and therefore insecticidal activity against pests
SQ Sequence 231 AA;
Query Match 98.8%; Score 1151; DB 2; Length 231;

04-APR-1991 (first entry)
 Mutant 27kD delta endotoxin.
 Mutant delta endotoxin; insecticide; mosquitoes; chimeric protein.
 Bacillus thuringiensis.
 US000875-H.
 01-JAN-1991.
 18-MAR-1988; 88US-00170211.
 18-MAR-1988; 88US-00170211.
 (DUPO) DU PONT DE NEMOURS & CO E I.
 Ellar DJ, Ward ES;
 WPI, 1991-028850/04.
 Nucleic acid fragments encoding mutant 27 KD delta endotoxins - from
 Bacillus thuringiensis var. israelensis, have improved insecticidal
 properties, part. against mosquitoes.
 Disclosure; Fig 1; 14pp; English.
 This mutant 27 kD delta endotoxin has a single amino acid substit- ution
 (Arg-78 to Ala) in the wild-type sequence. This results in a soluble
 insecticidal protein with improved insecticidal properties, e.g. lower
 haemolytic activity and greater expression in cells contg. sig. amts. of
 phosphatidate-type toxin receptors. It is hence useful e.g. against
 mosquitoes. See also AAR10853, AAR10282 and AAR10309

Query Match 38.6%; Score 450; DB 2; Length 249;
 Best Local Similarity 45.2%; Pred. No. 2.le-35;
 Matches 98; Conservative 44; Mismatches 55; Indels 10; Gaps 5;

5 RVITLTGPS-SDVNYSEIYQV-APQYVNOALTAKYFQGA-----DGSTLRFPDEKA 56
 25 RVITLRVEDPNEINLLSINEIDNPYILQAIMLANAFQNALVPTSTDFGDALFSPMPKG 84
 57 LOIANDI-PQAAVNTLNQTVQOGTVQSVSMIDKIVDMKNVLSIVIDNKKFWDQVTAAI 119
 85 LEIANTITPMGAVSYVDQNTQTNNQVSMINKVLEVLKTVLGVLSGSGSVI-DQLTAAV 143
 116 TMTFNLNSQSEAWIFYYKEDAHKTSYYYNILFAIQDEETGGVMATLPIAFDISVDIEK 175
 144 TMTFNLNTQKNEAWIFWGETANQNTYTNVLFATQNAQTGGVMYCPVGVFEIKVSARK 203
 176 EKLVFTIKDTENYAVTVKAINVVQALQSSRDSKVD 212
 204 EQVLFETIQDSASVNNVNIQSLKFAQPLVSSSTQYPIAD 240

RESULT 6
 AAR10309
 ID AAR10309 standard; protein; 249 AA.
 AC AAR10309;
 04-APR-1991 (first entry)
 Mutant 27kD delta endotoxin.
 Mutant delta endotoxin; insecticide; mosquitoes; chimeric protein.
 Bacillus thuringiensis.

PN US000875-H.
XX 01-JAN-1991.
XX 18-MAR-1988; 88US-00170211.
XX 18-MAR-1988; 88US-00170211.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Ellar DJ, Ward ES;
XX WPI; 1991-028850/04.
XX Nucleic acid fragments encoding mutant 27 KD delta endotoxins - from
PT Bacillus thuringiensis var. israelensis, have improved insecticidal
PT properties, part. against mosquitoes.
PS Disclosure; Fig 1; 14pp; English.
XX This mutant 27 kD delta endotoxin has a single amino acid substit- ution
CC (Lys-124 to Ala) in the wild-type sequence. This results in a soluble
CC insecticidal protein with improved insecticidal properties, e.g. lower
CC haemolytic activity and greater expression in cells contg. sig. ants. of
CC phosphatidate-type toxin receptors. It is hence useful e.g. against
CC mosquitoes. See also AAR10853 and AAR10282-83
XX
XX Sequence 249 AA;
Query Match 38.6%; Score 450; DB 2; Length 249;
Best Local Similarity 45.2%; Pred. No. 2.6e-35;
Matches 98; Conservative 44; Mismatches 65; Indels 10; Gaps 5;
Qy 5 RVITLTVPSS-SDVNVYSIYQV-APQYVNOALTILAKYFQGA------DGSTLRPFDEKA 56
Db 25 RVITLRVEDPNEINLLSINEIDNPNYILQAIMLANAFONALVPTSTDFGDALRFSMPKG 84
Qy 57 LOIANDI-PQAAVNTLNQTVQGVSVMDIKVIDMKVLSIVIDNKKFWDQVTAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSMINKVLEVLATVLGVALSGSVI-DQLTA 143
Qy 116 TMTFTNLNSQSEAWIFYYKEDAHKTSYYNINLFAIQDEETGGVMATLPIAFDISVDIEK 175
Db 144 TMTFTNLNTQNEAWIFMGKETANTQNTYTNVLFPAIQNAQTGGVMYCVPGVFEIKVSAVK 203
Qy 176 EKLVFTTIKTENYAVTVKAINVVQALQSSRDSKVD 212
Db 204 EQVLFTTQDSASVNVNIQSLKFAQPLVSSSTQYPIAD 240
RESULT 7
AAR24023
ID AAR24023 standard; peptide; 220 AA.
AC AAR24023;
XX 25-NOV-1992 (first entry)
DT Anticancer agent.
DE Thermochemotherapy; Bacillus thuringiensis.
XX Bacillus sp.
XX JP04128240-A.
XX 28-APR-1992.
XX 03-SEP-1990; 90JP-00232943.
XX 25-JUN-1990; 90JP-00166071.
XX (TONG) TOA GOSEI CHEM IND LTD.
PA

XX WPI; 1992-190107/23.
XX Anticancer agent for thermo-chemotherapy - contains polypeptide produced
PT from bacillus, and is pref. used with phloeoeycin.
XX Disclosure; Fig 1; 5pp; Japanese.
XX The sequence given is an anticancer agent for thermochemotherapy and has
CC a molecular weight of 25000. This protein is very efficient esp. when
CC used together with phloeoeycin and chemotherapy. This anticancer agent
CC is pref. isolated from Bacillus thuringiensis
XX
XX Sequence 220 AA;
Query Match 38.0%; Score 442.5; DB 2; Length 220;
Best Local Similarity 44.9%; Pred. No. 1.2e-34;
Matches 93; Conservative 44; Mismatches 61; Indels 9; Gaps 4;
Qy 14 SDVVNYSEIYQV-APQYVNOALTILAKYFQGA------DGSTLRPFDEKALQIANDI-PQ 65
Db 6 NEINLLSINEIDNPNYILQAIMLANAFONALVPTSTDFGDALRFSMPKGLEIANTITPM 65
Qy 66 AAVNTLNQTVQGVSVMDIKVIDMKVLSIVIDNKKFWDQVTAI-TNTFTNLNSQ 125
Db 66 GAVSVYDQNTQTNNQVSMINKVLEVLATVLGVALSGSVI-DQLTA 124
Qy 126 ESEAWIFYYKEDAHKTSYYNINLFAIQDEETGGVMATLPIAFDISVDIEKSVLFTIKD 185
Db 125 KNEAWIFMGKETANTQNTYTNVLFPAIQNAQTGGVMYCVPGVFEIKVSAVKEQVLFFTIQD 184
Qy 186 TENYAVTVKAINVVQALQSSRDSKVD 212
Db 185 SASVNVNIQSLKFAQPLVSSSTQYPIAD 211
RESULT 8
AAP90062
ID AAP90062 standard; peptide; 218 AA.
XX AAP90062;
AC AAP90062;
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 09-AUG-1990 (first entry)
XX Peptide with anticancer activity.
XX Anticancer agent; enhancer.
XX Bacillus thuringiensis serovar israelensis; ONR-60A.
XX JP01104019-A.
XX 21-APR-1989.
XX 29-JUL-1988; 88JP-00188207.
XX 31-JUL-1987; 87JP-00190347.
XX (TOAG) TOA GOSEI CHEM IND LTD.
XX WPI; 1989-161673/22.
XX Anticancer agents - contain polypeptide enhancer produced by Bacillus
PT microorganism.
XX Claim 1; Fig 6; 7pp; Japanese.
XX The polypeptide has anticancer activity and is capable of synergistically
CC enhancing other agents such as bleomycin, adriamycin, 5-FU and esp.
CC neocarzinostatin and thio-TEPA. See also J01104018. (Updated on 25-MAR-
CC 2003 to correct PF field.) (Updated on 24-OCT-2003 to standardise OS

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVQAALTLAKYFOGAI-----DGSTLRDPDE 54
 DB 38 RVIYLKV--KPIDTTQLLEITEIENPNVYLQALAAAFQDALVPTETFEGEAIRFSMP 95
 QY 55 KALQIANDI-POAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
 DB 96 KGLEVAKTIQPGAVVAYTDTQLSQSNQVSMIDRVISVLKTVMGVALSG-SIITQLTA 154
 QY 114 AITNTFTNLNSQSEAWIFYKKEDAKHTSYVYNILFAIQDEETGVMATLPIAFDISVDI 173
 DB 155 AITDTFTNLNTQKDSAWFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGEIRVFT 214
 QY 174 EKEKVLFTVTKDNYAVTVKAINVVQALQSRSDSKVVD---AFKSPRHL 220
 DB 215 DKRTVLFITTKDYANYSVNIQTLEFAQLIDSRALSINDLSEALRSSKYL 264

RESULT 11
 ID AA07850
 XX AA07850 standard; protein; 265 AA.
 AC AA07850;
 XX
 DT 17-OCT-2003 (revised)
 DT 27-AUG-1997 (first entry)
 XX
 DE Delta-endotoxin.
 XX
 KW Delta-endotoxin; Bacillus thuringiensis; gram-positive bacteria; mirid;
 KW spore forming bacteria; parasporal crystalline protein; Lygus hesperus;
 KW hemipteran insect; insect pest; crop pest; leaf bug; Lygus lineolaris;
 KW pesticide.
 XX
 OS Bacillus thuringiensis; strain PS20176.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..43
 FT /note= "removed to create activated truncated endotoxin"
 FT Protein 44..265
 FT /note= "mature activated delta-endotoxin"
 FT
 FN W09639843-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009987.
 XX
 PR 07-JUN-1995; 95US-00475924.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Stockhoff B, Conlan C;
 XX
 DR WPI; 1997-051641/05.
 DR N-PSDB; AAT47253.
 XX
 PT Biological control of hemipteran insect pests - using Bacillus
 PT thuringiensis delta-endotoxin, prof. expressed by transformed plants.
 XX
 PS Disclosure; Page 19-20; 28pp; English.
 XX
 CC This sequence represents the delta-endotoxin of Bacillus thuringiensis
 CC (B.t.) isolate PS20176. B.t. is a gram-positive, spore forming bacterium
 CC characterised by parasporal crystalline protein inclusions. The proteins
 CC can be highly toxic to pests and are specific in their toxic activity,
 CC and include the delta-endotoxins. The crystalline toxins are generally
 CC recognised as being protoxins, requiring either particular physicochemical
 CC conditions or the action of certain proteases to generate an active

CC toxin. This protein sequence is activated by the removal of 43 N-terminal
 CC amino acids. The protein can be used in the method of the invention. The
 CC method of the invention is for controlling hemipteran insect pests. The
 CC method comprises the administration of a B.t. delta-endotoxin to the
 CC pests or their environment. Of the hemipteran insect pests, the mirids
 CC (including Lygus) are the most notorious crop pests. The endotoxin
 CC encoded by this sequence is especially useful for controlling the leaf
 CC bugs Lygus hesperus and L. lineolaris. The method provides an
 CC environmentally acceptable alternative to the use of chemical pesticides.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 265 AA;

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

QY 5 RVITLTPSSDVVNYSEIYQVA---POYVQAALTLAKYFOGAI-----DGSTLRDPDE 54
 DB 38 RVIYLKV--KPIDTTQLLEITEIENPNVYLQALAAAFQDALVPTETFEGEAIRFSMP 95
 QY 55 KALQIANDI-POAAVNTLNQTVQGVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTA 113
 DB 96 KGLEVAKTIQPGAVVAYTDTQLSQSNQVSMIDRVISVLKTVMGVALSG-SIITQLTA 154
 QY 114 AITNTFTNLNSQSEAWIFYKKEDAKHTSYVYNILFAIQDEETGVMATLPIAFDISVDI 173
 DB 155 AITDTFTNLNTQKDSAWFWGKETSHTQNTYTNVWFALQNETTGRVMMCVPIGEIRVFT 214
 QY 174 EKEKVLFTVTKDNYAVTVKAINVVQALQSRSDSKVVD---AFKSPRHL 220
 DB 215 DKRTVLFITTKDYANYSVNIQTLEFAQLIDSRALSINDLSEALRSSKYL 264

RESULT 12
 AAY01207
 ID AAY01207 standard; protein; 265 AA.
 XX AAY01207;
 AC AAY01207;
 XX
 DT 20-MAR-2003 (revised)
 DT 25-MAY-1999 (first entry)
 XX
 DE B. thuringiensis PS20176 30kD delta-endotoxin.
 XX
 KW Hemipteran; insect; pest; Bacillus thuringiensis; delta-endotoxin;
 KW Lygus hesperus; Lygus lineolaris; insecticide; chemical pesticide;
 KW insect management; insecticide resistance.
 XX
 OS Bacillus thuringiensis.
 XX
 FN US5885963-A.
 XX
 PD 23-MAR-1999.
 XX
 PF 07-JUN-1996; 96US-00657579.
 XX
 PR 07-JUN-1995; 95US-00475924.
 XX
 PA (MYCO) MYCOGEN CORP.
 XX
 PI Conlan C, Stockhoff B;
 XX
 DR WPI; 1999-228582/19.
 DR N-PSDB; AAX26294.
 XX
 CC New method of killing hemipteran insect pests - by administration of a
 CC Bacillus thuringiensis delta-endotoxin from the B. thuringiensis isolate
 CC PS123DL, deposited in NRRL B-21011.
 XX
 PS Example; Col 15-16; 10pp; English.
 XX
 CC The invention relates to killing hemipteran insect pests by administering

CC a *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate
CC PS123D1, deposited in NRRL B-21011. The hemipteran insect pests that can
CC be controlled by the method are specifically Lygus hesperus and Lygus
CC lineolaris. The method provides an alternative to control of hemipteran
CC pests with chemical pesticides, allowing more environmentally-friendly
CC insect management and provides a tool for management of insecticide
CC resistance. The present sequence represents an approximately 30kd delta-
CC endotoxin of *B. thuringiensis* isolate PS201T6. (Updated on 20-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 265 AA;

RESULT 13	
AAR70755	
ID	AAR70755 standard; protein; 222 AA.
XX	
AC	AAR70755;
XX	
DT	16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	15-AUG-1995 (first entry)
XX	
DE	Delta-endotoxin 201T6 truncation.
XX	
XX	Delta-endotoxin; crystal protein; insecticide; pesticide;
KW	biological control agent; pest control; yellow fever mosquito;
KW	Aedes aegypti; housefly; Musca domestica; leafmining fly;
KW	Liriomyza trifolii; Western corn rootworm; Diabrotica virgifera;
XX	dipteran insect.
XX	
OS	Bacillus thuringiensis; var. neoleoensis.
XX	
PN	W09502693-Al.
XX	
PD	26-JAN-1995.
XX	
PF	14-JUL-1994; 94WO-US007887.
XX	
PR	15-JUL-1993; 93US-00093199.
PR	30-SEP-1993; 93US-00129610.
XX	
PA	(MYCO) MYCOGEN CORP.
XX	
PI	Payne J, Narva KE, Uyeda KA, Stalder CJ, Michaels TE;
XX	
WPI	1995-067337/09.
DR	N-PSDB; AAQ85361.
XX	
XX	
PT	Delta endotoxins produced by Bacillus thuringiensis isolates - are active
PT	against dipteran and/or corn rootworm.
XX	
PS	Claim 5; Page 33-34; 38pp; English.
XX	

[illegible]

RESULT 14	
AAR91967	
ID	AAR91967 standard; protein; 222 AA.
XX	
AC	AAR91967;
XX	
DT	16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	18-JUL-1996 (first entry)
XX	
XX	Truncated PS201T6 30 kDa toxin.
DE	
XX	
KW	Toxin; bacillus thuringiensis; PS201T6; cockroach; insecticide.
XX	
OS	Bacillus thuringiensis; isolate PS201T6.
XX	
XX	US5489432-A.
XX	
PD	06-FEB-1996.
XX	
XX	30-SEP-1993; 93US-00129609.
PF	
XX	
XX	06-NOV-1991; 91US-00788654.
PR	
PR	19-OCT-1992; 92US-00958551.
XX	
XX	(MYCO) MYCOGEN CORP.
PA	
XX	
XX	Schnepf HE, Brower DO, Kennedy MK, Payne JM, Randall JB;
PI	
XX	
XX	WPI; 1996-115589/12.
DR	
DR	N-PSDB; AAT16027.
XX	
XX	New purified toxin active against cockroaches - produced by a culture of
PT	Bacillus thuringiensis isolate PS201T6, has a mol. wt. less than 31 kD.
PT	
XX	
XX	Claim 1; Col 19-22; 12pp; English.
XX	
CC	This sequence represents a truncated form of the 30 kDa Bacillus
CC	thuringiensis (B.t.) toxin (see AAR91966), which is active against
CC	cockroaches. The encoding sequence was obtained from the B.t. isolate
CC	PS201T6, using the primers represented by AAT16031 and AAT16032. The
CC	

CC toxin has a high activity against cockroaches, while not affecting humans
 CC or animals. Insecticides such as this can be safely used in homes and
 CC restaurants. These insecticides will also be effective against strains
 CC resistant to currently used insecticides. The B.t. isolate PS201T6 may
 CC also be used directly to control the cockroaches. (Updated on 25-MAR-2003
 CC to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 222 AA;

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Query Match      35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVNYSYIYQVA-PQYVNOALTAKYFOGAI-----DGSTLRDFEFKALQIANDI-POA 66
Db 6 DTTQLLEITEIENPNYVLQALAAAFQDALVPPTETEFGEAIRFSMPKGLVAKTIQPKG 65
Qy 67 AVNTLNTQVQGTQVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
Db 66 AVAYTDTQLSQSNQVSMIDRVISVLKTVMGVALSG-SIITQLTAITDTFTNLNTQK 124
Qy 127 SEAMIFYYKEDAHKTSYYNYNLPALQIDBEETGGVMATLPIDFISVDIEKEKVLFTTKDT 186
Db 125 DSAWVFGKETSHTQNTYTNVMFAIQNETTGRVMMCVPIGPEIRVFTDKRTVLFLLTKDY 184
Qy 187 ENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 185 ANYSVNIQTLRPAQLIDSRALSINDLSEALRSSKYL 221

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RESULT 15
RAY01208
ID  AAY01208 standard; protein; 222 AA.
XX
XX  AAY01208;
XX
XX  20-MAR-2003 (revised)
XX  25-MAY-1999 (first entry)
XX
XX  B. thuringiensis PS201T6 truncated delta-endotoxin.
XX
XX  Hemipteran; insect; pest; Bacillus thuringiensis; delta-endotoxin;
XX  Lygus hesperus; Lygus lineolaris; insecticide; chemical pesticide;
XX  insect management; insecticide resistance.
XX
XX  Bacillus thuringiensis.
XX
XX  US5885963-A.
XX
XX  23-MAR-1999.
XX
XX  07-JUN-1996; 96US-00657579.
XX
XX  07-JUN-1995; 95US-00475924.
XX
XX  (MYCO ) MYCOGEN CORP.
XX
XX  Conlan C, Stockhoff B;
XX
XX  WPI; 1999-228582/19.
XX
XX  New method of killing hemipteran insect pests - by administration of a
XX  Bacillus thuringiensis delta-endotoxin from the B. thuringiensis isolate
XX  PS123DI, deposited in NRRL B-21011.
XX
XX  Example; Col 17-18; 10pp; English.
XX
XX  The invention relates to killing hemipteran insect pests by administering
XX  a Bacillus thuringiensis delta-endotoxin from B. thuringiensis isolate
XX  PS123DI, deposited in NRRL B-21011. The hemipteran insect pests that can
XX  be controlled by the method are specifically Lygus hesperus and Lygus
XX  lineolaris. The method provides an alternative to control of hemipteran
XX  pests with chemical pesticides, allowing more environmentally-friendly

```

CC insect management and provides a tool for management of insecticide
 CC resistance. The present sequence represents a truncated delta-endotoxin
 CC of B. thuringiensis isolate PS201T6 of about 25 kb. (Updated on 20-MAR-
 CC 2003 to correct PF field.)
 XX

SQ Sequence 222 AA;

```

Query Match      35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVNYSYIYQVA-PQYVNOALTAKYFOGAI-----DGSTLRDFEFKALQIANDI-POA 66
Db 6 DTTQLLEITEIENPNYVLQALAAAFQDALVPPTETEFGEAIRFSMPKGLVAKTIQPKG 65
Qy 67 AVNTLNTQVQGTQVSVMDIKVIDIMKNVLSIVIDNKKFWDQVTAITNTFTNLNSQE 126
Db 66 AVAYTDTQLSQSNQVSMIDRVISVLKTVMGVALSG-SIITQLTAITDTFTNLNTQK 124
Qy 127 SEAMIFYYKEDAHKTSYYNYNLPALQIDBEETGGVMATLPIDFISVDIEKEKVLFTTKDT 186
Db 125 DSAWVFGKETSHTQNTYTNVMFAIQNETTGRVMMCVPIGPEIRVFTDKRTVLFLLTKDY 184
Qy 187 ENYAVTVKAINVVQALQSSRDSKVVD---AFKSPRHL 220
Db 185 ANYSVNIQTLRPAQLIDSRALSINDLSEALRSSKYL 221

```

Search completed: June 26, 2005, 16:02:31
 Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:56:03 ; Search time 40 Seconds
(without alignments)
555.652 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFNFRVILTVSPSSDVVNS.....DAFKSPRLPRKHKICSNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	637	54.7	259	2 S32432	toxin cytB - Bacil
2	456	39.1	249	2 A27520	28K crystal protei
3	456	39.1	249	2 A24044	28K parasporal cry
4	103	8.8	477	2 E64595	hypothetical prote
5	101	8.7	477	2 F71918	hypothetical prote
6	99.5	8.5	4540	2 T30838	cytoplasmic dynein
7	96.5	8.3	343	2 A41874	transcription repr
8	95.5	8.2	201	2 A34146	hypothetical prote
9	95.5	8.2	421	1 F64205	thymidine phosphor
10	95.5	8.2	1876	2 E97944	zinc metalloprotei
11	94.5	8.1	249	2 A33963	hypothetical prote
12	94.5	8.1	393	2 S69708	26S proteasome reg
13	92.5	7.9	4688	2 F82885	hypothetical prote
14	91	7.8	458	2 E65068	hypothetical prote
15	89.5	7.7	311	2 T32776	hypothetical prote
16	89.5	7.7	1363	2 C84346	hypothetical prote
17	89	7.6	772	1 JQ2026	outer layer protei
18	89	7.6	1017	2 D90550	hypothetical TPR d
19	89	7.6	1389	2 T41230	vsaa-like (mycopla
20	89	7.6	1805	1 A64224	hypothetical prote
21	88.5	7.6	717	2 T28247	ORF MSV086 probab
22	88.5	7.6	735	2 D70174	methyl-accepting c
23	88.5	7.6	1447	2 F82909	hypothetical prote
24	88	7.6	458	2 E91092	probable invasion
25	88	7.6	458	2 A85938	probable invasion
26	88	7.6	646	2 A91587	bacteriophage prot
27	87.5	7.5	1636	2 S60403	probable membrane
28	87	7.5	390	2 S54026	ribosomal protein
29	87	7.5	488	2 T33739	hypothetical prote

30	87	7.5	653	2 A29821	dnak-type.molecula
31	87	7.5	853	2 G90559	trse-like protein
32	86.5	7.4	382	2 A48492	polyaaccharide exp
33	86.5	7.4	474	2 G83507	flagellar capping
34	86.5	7.4	1418	2 S64918	hypothetical prote
35	86	7.4	739	2 H75001	methyl-accepting c
36	86	7.4	1237	2 AC1583	internalin protein
37	86	7.4	1595	2 T31082	endo-1,4-beta-xyla
38	85.5	7.3	518	2 F86814	bifunctional purin
39	85.5	7.3	1465	2 A70199	hypothetical prote
40	85.5	7.3	1648	2 S57163	probable membrane
41	85.5	7.3	2599	2 P90608	ABC transporter pe
42	85	7.3	236	2 D84969	basal-body rod mod
43	85	7.3	320	2 F69527	ISA1214-6 transpos
44	85	7.3	537	2 A35400	surface protein T6
45	85	7.3	640	2 T03754	hypothetical prote

ALIGNMENTS

RESULT 1

S32432
toxin cytB - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32432; S31476
R:Koni, P.A.; Ellar, D.J.
J: Mol. Biol. 229, 319-327, 1993
A:Title: Cloning and characterization of a novel Bacillus thuringiensis cytolytic delta
A:Reference number: S32432; MUID:93156045; PMID:8429550
A:Accession: S32432
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KON>
A:Cross-references: UNIPROT:Q04470; EMBL:Z14147; NID:G49305; PIDN:CAA78519.1; PID:G49307
C:Genetics:
A:Gene: cytB
C:Superfamily: 28K parasporal crystal protein

Query Match 54.7%; Score 637; DB 2; Length 259;
Best Local Similarity 56.0%; Pred. No. 1.2e-43;
Matches 126; Conservative 43; Mismatches 54; Indels 2; Gaps 2;

QY	7	ITLTVPSDDVNSIYVAPQYVNOALTAKYFQGAIDGSLRFDPEKALQIANDIPOA	66
DB	31	IVLTVPSSDLNFWTVFVQPOYINQALHLANAFQGAIDPLNLFNFEKALQIANGIPNS	90
QY	67	AVVNTLNTQVQGTQVQSVMDIKYDVMKNVLSIVIDNKKFWDQVTAATNTFTTNLSQE	126
DB	91	AIKVTLNSQSVIQQTVEISVWVEQLKKIIQEVGLGVNSTSPWNSVEATIKGTFTNLDTOI	150
QY	127	SEAWTFYKEDAKHTSYNYNLFALQDEETGCGWMTLPADFISVDIEKEKLVFTIKOT	186
DB	151	DEAWTFWHSLSAHTSYNYNLFISIQNEDTGAVMAVPLAFESVDVEKQVLFFTIKDS	210
QY	187	ENYAVTVKAINVQALQSRSQKVYDAFK-SPRHLPRKHKICSN	230
DB	211	ARYEVKMAKTLVQALHSS-NAPIVDIFNVNNYLYHSHKLIQN	254

RESULT 2

A27520
28K crystal protein - Bacillus thuringiensis plasmide
N:Alternate names: 28K cytolytic protein; delta-endotoxin
C:Species: Bacillus thuringiensis
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A27520; S06430
R:Earp, D.J.; Ellar, D.J.
Nucleic Acids Res. 15, 3619, 1987
A:Title: Bacillus thuringiensis var. morrisoni strain PG14: nucleotide sequence of a ge
A:Reference number: A27520; MUID:87203386; PMID:3575104
A:Accession: A27520

A;Molecule type: DNA
A;Residues: 1-249 <EAB>
A;Cross-references: UNIPROT:P05069; GB:Y00135; NID:940260; PIDN:CAA68329.1; PID:G40261
A;Experimental source: strain morrissoni PG14, 140kb plasmid
R;Galjart, N.J.; Sivaseubramanian, N.; Federici, B.A.
Curr. Microbiol. 16, 171-177, 1987
A;Title: Plasmid location, cloning, and sequence analysis of the gene encoding a 27.3-kDa
A;Reference number: S06430
A;Accession: S06430
A;Molecule type: DNA
A;Residues: 1-249 <GAL>
A;Cross-references: EMBL:M35968; NID:G143104; PIDN:AAA22553.1; PID:G143105
C;Genetics:
A;Genome: plasmid
C;Superfamily: 28K parasporal crystal protein
C;Keywords: delta-endotoxin

Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 3.4e-29;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
Qy 5 RVITLTVPSS-SDVNVSEIYQV-APQYVNOALTAKYFQGA-----DGSTLRPFDFEKA 56
Db 25 RVITLRVEDPNEINLLSINEIDNPNTYILQAILANAFQNALVPTSTDFGDALRFSMAKG 84
Qy 57 LQIANDI-PQAAVNTLNQTVQOQTVQVSMIDKIVDMKIVLSIVIDNKKFWDQVTAAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSMINKVLELVLTGLVGLVSGSVI-DQLTAAV 143
Qy 116 TMTFTNLNSQSEAWIFYKEDAHKTSYYNINLFAIQDEETGGVNMATPIAFDISVDIEK 175
Db 144 TMTFTNLNTQKNEAWIFWGKETANTQNTYNNVLFALQNAQTGGVMYCVPGVEIKVSARK 203
Qy 176 EKVLFTVTKIDTENYAVTVKAINVVQALQSSRDSKVVD 212
Db 204 EQLVFTTQDSASYNVNIQSLKFAQLPVSSSQYPIAD 240

RESULT 3
A24044
28K parasporal crystal protein precursor - Bacillus thuringiensis subsp. israelensis
N;Alternate names: delta-endotoxin
N;Contains: 24K parasporal crystal protein; 25K parasporal crystal protein
C;Species: Bacillus thuringiensis subsp. israelensis
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24044; A60123; A24505; S02651
R;Waaijijk, C.; Dullenans, A.M.; van Workum, M.E.S.; Visser, B.
Nucleic Acids Res. 13, 8207-8217, 1985
A;Title: Molecular cloning and the nucleotide sequence of the Mr 28,000 crystal protein
A;Reference number: A24044; MUID:86067227; PMID:4070003
A;Accession: A24044
A;Molecule type: DNA
A;Residues: 1-249 <WAA>
A;Cross-references: UNIPROT:P05069
A;Note: the authors translated the codon GAA for residue 204 as Gln
R;Gill, S.S.; Singh, G.J.P.; Hornung, J.M.
Infect. Immun. 55, 1300-1308, 1987
A;Title: Cell membrane interaction of Bacillus thuringiensis subsp. israelensis cytolytic
A;Reference number: A60123; MUID:87193126; PMID:3570465
A;Accession: A60123
A;Molecule type: protein
A;Residues: 31-41 <GLI>
A;Note: this amino-terminal sequence was found in both 24K and 25K forms of the purified
R;Ward, E.S.; Ellar, D.J.
J. Mol. Biol. 191, 1-11, 1986
A;Title: Bacillus thuringiensis var. israelensis delta-endotoxin. Nucleotide sequence and
A;Reference number: A24505; MUID:87086764; PMID:3025452
A;Accession: A24505
A;Molecule type: DNA
A;Residues: 1-249 <WARI>
R;Ward, E.S.; Ellar, D.J.; Chilcott, C.N.
J. Mol. Biol. 202, 527-535, 1988
A;Title: Single amino acid changes in the Bacillus thuringiensis var. israelensis delta-

A;Reference number: S02651; MUID:89011977; PMID:2845100
A;Accession: S02651
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-249 <WAR2>
C;Comment: This protein is one of several from the parasporal protein inclusion that set
C;Superfamily: 28K parasporal crystal protein
C;Keywords: delta-endotoxin
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-249/Product: 28K parasporal crystal protein #status experimental <WAT>

Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 3.4e-29;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
Qy 5 RVITLTVPSS-SDVNVSEIYQV-APQYVNOALTAKYFQGA-----DGSTLRPFDFEKA 56
Db 25 RVITLRVEDPNEINLLSINEIDNPNTYILQAILANAFQNALVPTSTDFGDALRFSMPKG 84
Qy 57 LQIANDI-PQAAVNTLNQTVQOQTVQVSMIDKIVDMKIVLSIVIDNKKFWDQVTAAI 115
Db 85 LEIANTITPMGAVSVYDQNTQTNNQVSMINKVLELVLTGLVGLVSGSVI-DQLTAAV 143
Qy 116 TMTFTNLNSQSEAWIFYKEDAHKTSYYNINLFAIQDEETGGVNMATPIAFDISVDIEK 175
Db 144 TMTFTNLNTQKNEAWIFWGKETANTQNTYNNVLFALQNAQTGGVMYCVPGVEIKVSARK 203
Qy 176 EKVLFTVTKIDTENYAVTVKAINVVQALQSSRDSKVVD 212
Db 204 EQLVFTTQDSASYNVNIQSLKFAQLPVSSSQYPIAD 240

RESULT 4
B64595
hypothetical protein HP0605 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B64595
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Katpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64595
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-477 <TOM>
A;Cross-references: UNIPROT:O25326; GB:AE000574; GB:AE000511; NID:G2313721; PIDN:AAD07671

Query Match 8.8%; Score 103; DB 2; Length 477;
Best Local Similarity 20.5%; Pred. No. 1.3;
Matches 47; Conservative 54; Mismatches 90; Indels 38; Gaps 10;
Qy 2 PFN---RVITLTVP---SSDVNVSEIYQVAPQYVNOALTAKYFQGA---DGSTLRPF 51
Db 199 YFNRLARMLAQKLEQIKTDIKRVTKLYDKGLTTDIDLQSLKA--QGNLSEYDILDWQF 256
Qy 52 DFEKALQIANDIPQAAVNTLNQTVQOQTVQVSMIDKIVDMKIVLSIVIDNKKFWDQV 111
Db 257 ALEQNRLTLEVLTNLSVKNLTKTTIDAPNLQLRERQD-LVSLREQISAIRYQNKQL--- 311
Qy 112 TAAITNTFTNLNSQSEAWIFYKEDAHKTSYYNINLFAIQDEETGGVNMATPIAFDISV 171
Db 312 ----NYPKIDVFDSS--WLFWIQKPAVATGRFGN--FYPGQONTAGTATLNIIPDDIGL 362
Qy 172 DIEKEKVLFTVTKIDTENYA-----VTVKAINVQVA-LOSSRDS 208
Db 363 SLQKQSIMLGQLANEKNLAYKKLQKDEQLYRKSLDIPARAKIESKAS 411

[illegible]

RESULT 7
A41874
transcription repressor of class I heat-shock gene hrca - Bacillus subtilis
N:Alternate names: hypothetical protein 39
C:Species: Bacillus subtilis
C>Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A41874; G65642; S57503
R:Wetzstein, M.; Voelker, U.; Dedio, J.; Loebau, S.; Zuber, U.; Schlesswohl, M.
J. Bacteriol. 174, 3300-3310, 1992
A:Title: Cloning, sequencing, and molecular analysis of the dnaK locus from Bac
A:Reference number: A41874; MUID:92250426; PMID:1339421
A:Accession: A41874
A:Molecule type: DNA
A:Residues: 1-343 <WET>
A:Cross-references: UNIPROT:P25499; EMBL:M84964; NID:gl43056; PIDN:AAA22526.1;
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, J.
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carver, C.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Fer
Nature 390, 249-256, 1997

A: Techn, G.; Harwood, C.K.; Renaud, A.; Krogh, S.; Kumano, M.; Kurita, K.; Hosono, S.; Koetter, P.; Koningsreick, G.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, A.; Authors: Lauber, J.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Fiebig, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, M.; Sadale, J.; Sato, T.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sekiguchi, Y.; Sekowska, A.; Authors: Schlecht, S.; Schroeter, R.; Scoffone, F.; Segkuchi, J.; Tanaka, V.; Ikeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; t.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus*
A:Reference number: A69580; PMID:98044033; PMID:9384377
A:Accession: G69642
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Cross-references: 1-343 <KUN>
A:Cross-references: GB:J299117; GB:AL009126; NID:G26349466; PIDN:CAB14491.1; PID
A:Experimental source: strain 168
C:Genetics:

A:Gene: hrcaA
C:Superfamily: conserved hypothetical protein MG205
C;Keywords: heat shock; stress-induced protein

	Query Match	8.3%	Score 96.5;	DB 2;	Length 343;	
	Best Local Similarity	20.7%;	Pred. No. 2.9;			
	Matches 47;	Conservative 38;	Mismatches 83;	Indels 59;	Gaps 8;	

Qy	14	SDVNTYSEI-----YQAPQYVNQAULTAKYFQGAGDSTLRP-----DF	53			
	:	:	:	:	:	:
	115	SDLTNYTSIVLGPKLSENYLKQIQIIPIQDMAVAILVTNTHGVENKTINFPTKMDSLDI	174			
Db						
Qy	54	EKALQIANDIPQAAVVNTLNQTVOOGTVQVSVMIDKIVDIMKNVLISVIDDNKKFWQVTA	113			
		:	:	:	:	:
	175	EKLUNIDRLNSGVPMDNELN-----IPKEVVMYLRQHIKNYDNIILD	217			
Db						


```
QY 7 ITLTPSSDVNYSYIYQVAPQVQVQALTLAKYFOGAI DSGTLRPD-----FEKA--LQ 58
Db 553 IKLALKDKDQGLVKEV-TVAENNINATLDKLYIQGYSTLTSTTMVYDRGSEBETEKLEDKQ 611
QY 59 IANDIPQAAVNV-----TLNQTVQOGTVQVSVWIDKIVDI-----MK 95
Db 612 IQLDLKKVEIKIKETSIMNVDAEGNETDKSLLSEKPTDVSQLYLRVTHDNKVRFLAVS 671
QY 96 NVLSIVINDKKFWDQVTAITNTFTNLNSQSEAWIFYYKEDAHK-TSYYYNILFAIQDE 154
Db 672 SVEEVVVDGKTLKYVAKAPDLVQRADDTLSEEVVHYPEKQLPKVNNVYVNFELVKDM 731
QY 155 ETGGVWATLPIAFDI-SVDIEKEKLVFV-----TIKDENVAVTV 193
Db 732 Q-ANPMGEFKGADLNAVNVNVPAGKAYVNAKFRGTLSSVENHQYTI 776

RESULT 11
A:39363
hypochemical protein BH2505 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
A:Accession: AB3963
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: AB3963
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q9K9Y9; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BA8062
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2505
C:Superfamily: conserved hypothetical protein y100; conserved hypothetical protein y100

Query Match 8.1%; Score 94.5; DB 2; Length 249;
Best Local Similarity 21.0%; Pred. NO. 2.7;
Matches 37; Conservative 38; Mismatches 64; Indels 37; Gaps 7;

QY 62 DIPQAAVNTLNQTVQOGTVQVSVMI-----DKIVDMKNVLSIVINDKKFWDQVTAI 115
Db 8 DVGKVRPNEDGTIMEXKQGLLVVADGMGQHQAQVASKMATELL--KEAWESAS--- 62

QY 116 TMTFTNLNSQSEAWIFYYKEDAHKTSYVYNILFAIQDEBTGGVWATLPIAFDISVDIEK 175
Db 63 -----LSPSQSEGLRQVHLVNESLHY-----AQKHECCGMGTTL-----VAAIVDK 109

QY 176 EKVLFVTIKDTENYAVTVKAINVQALQSSRDSKYVDAP-----KSPRHLPRK 223
Db 110 ERVTTAHIGDSRAYLLNEHGF-----QKTRDHSVLNVLVRTGQISDBEAHHPRK 160

RESULT 12
S69708
26S proteasome regulatory particle chain RPN9 - yeast (Saccharomyces cerevisiae)
A:Alternate names: protein YDR427W
C:Species: Saccharomyces cerevisiae
C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: S69708
R:Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 941
A:Reference number: S69555
A:Accession: S69708
A:Molecule type: DNA
A:Residues: 1-393 <DIE>
C:Cross-references: UNIPROT:Q04062; EMBL:U33007; NID:g927685; PID:g927687; GSPDB:GN00004
C:Genetics:
A:Gene: SGD:RPN9; RPN9; MIPS:YDR427W
A:Cross-references: MIPS:YDR427W; SGD:S0002835
A:Map position: 4R
```

```
Query Match 8.1%; Score 94.5; DB 2; Length 393;
Best Local Similarity 24.1%; Pred. NO. 4.9;
Matches 57; Conservative 42; Mismatches 83; Indels 55; Gaps 16;

QY 30 VNOALTAKYFOGAI DSGTLRPDPEKALQIANDIPQAAVNTLNQTVQOGTVQVS----- 84
Db 73 INQ-LSVVKYLLASLQSK---DFDESILYLDL--KAQFBLDSKKQRNNGSKKHGDGI 126
QY 85 VMIDKIV-----DIMK-----NVLSIVINDKKFWDQVTAITNTFTNLNSQSEAWI 131
Db 127 LLIDSEIARTYLLKNDLVKARDLLDLEKTLDKK---DSIPLRITNSFVSTNSQ-----Y 178
QY 132 FYYKEDAHKTSYVYNILFAIQDEBTGGVWATL-----PIAFDISVD-IEKEKV----- 178
Db 179 PKFNDFN--SPYYTSLLYLTLEP--STSITLAERQQLAYDLISALLGDKIYNFQELLH 235
QY 179 -LFTVITIKDTENYAVTVKAINVQALQSSR-DSKV-VDAPKSP-----RHLPRKHKIC 228
Db 236 HPIMETIVNDSNYDWLFQLNALTVGDFDKFSLIKVQISKIPILAQHSFLRQKIC 292

RESULT 13
P82895
hypochemical protein UU482 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m
A:Reference number: A82870
A:Accession: F82885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4688 <GLA>
A:Cross-references: GB:AS002145; GB:AF222894; NID:g6899476; PIDN:AAF30894.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU482
A:Genetic code: SGC3

Query Match 7.9%; Score 92.5; DB 2; Length 4688;
Best Local Similarity 22.3%; Pred. NO. 1.9e+02;
Matches 44; Conservative 32; Mismatches 72; Indels 49; Gaps 8;

QY 51 FDFEKAQIANDI-PQAAVNTLNQTVQOGTVQVSVWIDKIV---DIMKNVLSIVINDKK 106
Db 1509 YDEQNKISLNNINPTSYKPTINKNDKSVNIDVLDQVLDKOLLANQYLRLLKQLNDNKT 1568
QY 107 FW-DQV-----TAAITNTFTNLNSQSEAWIFYYKEDAHKTSYVYNILFAIQDEETGGVMA 161
Db 1569 VWTDPILPNNNAKISFKLSNL-----IHNRAVELEGLYYFDQNSVNDMT 1613
QY 162 TLPIAFDISV---DIEKEKLVFTIKDTENYAVTVKAIN-----VVQ 200
Db 1614 NNQISFNSKIHKPIETEPSPSLTTINYDTNNAIKTVSAHNAQVHFVKLTNDALENDQIVE 1673
QY 201 AL-----QSSRDSKVDA 213
Db 1674 AVFAPTNNLNDQKVVEA 1690

RESULT 14
E85068
hypochemical protein b2852 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: E85068
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
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